

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 5, 2004, 17:56:29 ; Search time 13.875 Seconds
(without alignments)
1282.249 Million cell updates/sec

Title: US-10-045-574B-27
Perfect score: 966
Sequence: 1 MRRGRPSLRGRDAPPTPCV.....ATELGSTELVTTKTAGPEQQ 185

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues
Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 76:*
1: P11:*
2: P12:*
3: P13:*
4: P14:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	118.5	12.3	416	1 SKXLAG	dermal gland prote
2	118	12.2	422	2 S32357	glial growth facto
3	117.5	12.2	552	2 T08148	proline-rich myros
4	116	12.0	676	1 EDBE23	immediate-early pr
5	115	11.9	356	1 WJH02H	homeotic protein H
6	114.5	11.9	862	2 T46289	hypothetical prote
7	106.5	11.0	505	2 S72273	actin-depolymerizi
8	105.5	10.9	2142	2 B35098	MHC class III hist
9	103.5	10.7	548	2 S52735	CW17R protein - mo
10	103.5	10.7	1487	1 EDBEF6	155K transcription
11	102.5	10.6	1487	1 EDBE1	immediate-early pr
12	102	10.6	676	1 EDBE22	immediate-early pr
13	102	10.6	3938	2 T42761	Bassoon protein -
14	101.5	10.5	815	2 B56708	extracellular sign
15	101.5	10.5	3436	2 S55659	tegument protein 6
16	101	10.5	801	2 T29018	hypothetical prote
17	101	10.5	896	2 S36326	clathrin assembly
18	101	10.5	915	2 S36327	clathrin assembly
19	101	10.5	1952	2 T48814	hypothetical prote
20	100.5	10.4	592	2 D70863	hypothetical prote
21	100.5	10.4	862	2 S51493	major nitrogen reg
22	99.5	10.3	839	2 F75518	hypothetical prote
23	99.5	10.3	1870	2 S37671	MHC class III hist
24	99.5	10.3	1872	2 S36152	MHC class III hist
25	98.5	10.2	347	2 F75353	hypothetical prote
26	98.5	10.2	639	2 G02319	transcription fact
27	98.5	10.2	1334	2 T50568	probable multi-dom
28	98	10.1	903	2 T00705	N-chimerin homolo
29	97.5	10.1	317	2 T19143	hypothetical prote

serine/threonine p
RXR-beta1 isoform
hypothetical prote
hypothetical prote
probable multi-dom
albumin D-box bind
cyclin-dependent k
drebrin E2 - chick
phosphoprotein, sy
Bassoon protein -
osteoblast specifi
hypothetical prote
regulatory protein
gene LF3 protein -
hypothetical prote
gene H0X2.8 protei

ALIGNMENTS

RESULT 1

SKXLAG
dermal gland protein APEG precursor - African clawed frog (fragment)
C:Species: Xenopus laevis (African clawed frog)
C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jun-2000
C:Accession: S07498: A34140
R:Gnathl, M.; Berger, H.; Thallhammer, J.; Kreil, G.
FEBS Lett. 260, 145-148, 1990
A>Title: Dermal glands of Xenopus laevis contain a polypeptide with a highly repetitive
A:Reference number: A34140; MUID:90127399; PMID:2298293
A:Accession: S07498
A:Molecule type: mRNA
A:Residues: 1-416 <GMA>
A:Cross-references: EMBL:X51394; NID:G64547; PIDN:CAA35759.1; PID:G1334643
A:Note: the authors translated the codon TTC for residue 8 as Pro
C:Superfamily: dermal gland protein APEG; trefoil homology
C:Keywords: skin; tandem repeat
F:1-20/Domain: signal sequence (fragment) #status predicted <SIG>
F:21-416/Product: dermal gland protein APEG #status predicted <WAT>
F:23-344/Region: alanine/glutamic acid/glycine/proline-rich repeats
F:349-389/Domain: trefoil homology <TRF>
F:349-375,359-374,369-386/Disulfide bonds: #status predicted

Query Match	12.3%	Score	118.5	DB	1	Length	416
Best Local Similarity	26.0%	Pred. No.	0.11				
Matches	44	Conservative	10	Mismatches	58	Indels	57
Gaps	7						
QY	12	DAPAPTEC-----VPAECFDLLVRHCVCAGLLRTPREKEXAG-ASSPAPRTALQPOES	63				
Db	163	EAPAPAEAGEAPAPAEAG-----EAPAPAEAGEAPAPAEAGEAPAPA	208				
QY	64	VGAGAGERALPLPGLLFGAPALLGLALVLVLVSVRRRRRLRGASSAEAP-DGDK	122				
Db	209	PAPAEAGEAPAPAPA-----EGEAPAPAEAGEA	236				
QY	123	DAPEPLD-KVILSPGISDATAPWPPGEGDPTTPGHSVVPATELG	170				
Db	237	PAPAPAEAGEAPAPAEAGEAPAPA-PAEAGEAPAPAEAGEAPAPAEAG	284				

RESULT 2

S32357
glial growth factor - human
C:Species: Homo sapiens (man)
C>Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 08-Sep-2002
C:Accession: S32357
R:Marchionni, M.A.; Goodearl, A.D.J.; Chen, M.S.; Birmingham-McDonogh, O.; Kirk, C.; Heles, I.; Davis, J.B.; Hsuan, J.J.; Totty, N.F.; Otsu, M.; McBurney, R.N.; Waterfield, M.
Nature 362, 312-318, 1993
A>Title: Glial growth factors are alternatively spliced erbB2 ligands expressed in the
A:Reference number: S32357; MUID:93205115; PMID:8096067
A:Accession: S32357

A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-422 <MAR>
A:Cross-references: GB:112260; NID:G992047; PIDN:AAB59622.1; PID:G292048
C:Superfamily: human heregulin; EGF homology; immunoglobulin homology
F:363-402/Domain: EGF homology <EGF>

Query Match 12.2%; Score 118; DB 2; Length 422;
Best Local Similarity 28.3%; Pred. No. 0.12; Mismatches 70; Gaps 11;
Matches 54; Conservative 16; Indels 51; Indels 70; Gaps 11;

QY 2 RRGSRSLGRDAPAPTCVPAECFDLLVRHCVAGLLRTPRPKPXAGASSPAP-----54
DB 4 RRAPRR-SGRPGP-----RAQRPGSARSPPLFLFLILL 38

QY 55 --RTALPQESVGAGAGEAALPL-PGLLFCAPALLG-----LALVALVLVGVSWRRQR 107
DB 39 LGTALAP-----GAAAGNEAPAGASVCYSSPSVSVQELAQRAAVVIEGKVHQRQQ 94

QY 108 ----RLRGASSAEP--DGDKDAPELDKVIILSPGISDATAP-AWPPPGEDP-----GT 155
DB 95 GALKDKAAAGAGAGWGWDREPP-----AAGPRALGPPAEFPLLAANGT 139

QY 156 TPGHSPVPVA 166
DB 140 VPSWPTAEVPS 150

RESULT 3
T08148
proline-rich myrosinase-binding protein homolog - rape (fragment)
N:Alternate names: myrosinase-binding protein related protein
C:Species: Brassica napus (rape)
C:Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 08-Oct-1999
C:Accession: T08148
R:Taipalensuu, J.; Falk, A.; Ek, B.; Rask, L.
Eur. J. Biochem. 243, 605-611, 1997
A:Title: Myrosinase-binding proteins are derived from a large wound-inducible and repetitive
A:Reference number: Z16379; MUID:97210758; PMID:9057822
A:Accession: T08148
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-352 <TAI>
A:Cross-references: EMBL:U59446; NID:G1655829; PIDN:AAC08051.1; PID:G165830
A:Experimental source: cv. 20516 of Svalof's Karat; immature seed, 30 days after pollination

Query Match 12.2%; Score 117.5; DB 2; Length 552;
Best Local Similarity 28.8%; Pred. No. 0.17;
Matches 49; Conservative 5; Mismatches 59; Indels 57; Gaps 9;

QY 22 ABCFDLLVRHCVACGLLRTPRPKPKXAGASGPAPRTALPQESVGAGAGEAALPLPGLLFG 81
DB 282 ADAIDALGAH---FGPLETPAPAP-----SPAGCPAPAPGSHPAPAPAPAGF-----329

QY 82 APALLGLALVALVLVGLVSWRRQRRLRGASSAEPD-GDKDAPBPLDKVILSPGISD 140
DB 330 -----QGRPAPAPGAGRPSPAP-----GFGPRP 354

QY 141 ATAPAWPPRGEDCGTTP---PG---HSVP--VPATELGSTELVTTKTAGP 182
DB 355 APAPA-PAPGQPRPAPGAPGQGFHPAPAAAPGTSATPAPATTYTKGP 403

RESULT 4
EB0E23
immediate-early protein IER2.9 - bovine herpesvirus 1 (strain Jura)
N:Alternate names: early protein ER2.6; p135 protein
C:Species: bovine herpesvirus 1
C:Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 17-Mar-2000
C:Accession: B38209
R:Wirth, U.V.; Praefel, C.; Vogt, B.; Vlcek, C.; Paces, V.; Schwyzer, M.
J. Virol. 66, 2763-2772, 1992
A:Title: Immediate-early RNA 2.9 and early RNA 2.6 of bovine herpesvirus 1 are 3' coterm

A:Reference number: A38209; MUID:92219360; PMID:1313901
A:Accession: B38209
A:Molecule type: DNA
A:Residues: 1-676 <WIR>
A:Cross-references: GB:M84465; NID:G330769; PIDN:AA46062.1; PID:G330770
C:Superfamily: herpesvirus immediate-early protein IE110; RING finger homology
C:Keywords: DNA binding; immediate-early protein; transcription regulation; zinc finger
F:9-57/Domain: RING finger homology <RNG>
F:13-51/Region: zinc finger C3HC4 motif
F:284-331/Region: acidic

Query Match 12.0%; Score 116; DB 1; Length 676;
Best Local Similarity 30.8%; Pred. No. 0.27; Mismatches 82; Indels 44; Gaps 10;
Matches 62; Conservative 13; Indels 82; Indels 44; Gaps 10;

QY 7 SLRGDAPAPTCVPAECFDLLVRHCVAC-----GLLFTPR-----PKPX 46
DB 353 SITEGRTPAVQAPRS---LARRPCGAAAVASPPSSRSGRDRPLPAAPRAAPAAQ 408

QY 47 AGASSPAPRTALPQESVGAGAGEAALPLPGLLFCAPALLGLVALVLVYG---LVSWR 103
DB 409 ARACSPPEPR-----EEGRGAGLGVAAAGTAGWAGSEEGRGERRARLLGEAGPPRVQARR 463

QY 104 RRORRL-RGASSAEPDGDKDAPELDKVIILSPGISDATA-PAWPPPGEDPGTTTPGHS 161
DB 464 RRTELDRAPTAPAP---APAPAPISTVIDLT---ANAPAPADPAPAAAPGASAGAQ 517

QY 162 VVPATELGSTELVTTKTAGP 182
DB 518 IGTPA-----AAAAVTAATAAP 534

RESULT 5
WJ02H
homeotic protein Hox B2 - human
N:Alternate names: homeotic protein Hox 2.8; homeotic protein Hox 2H; homeotic protein
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 22-Jun-1999
C:Accession: S07542; S00989; S15549; A56093; E37042; S44216
R:Acampora, D.; d'Esposito, M.; Paiella, A.; Pannese, M.; Migliaccio, E.; Morelli, F.;
Nucleic Acids Res. 17, 10385-10402, 1989
A:Title: The human HOX gene family.
A:Reference number: S07541; MUID:90098876; PMID:2574852
A:Accession: S07542
A:Molecule type: mRNA
A:Residues: 1-356 <ACA>
A:Cross-references: EMBL:X15665; NID:G32381; PIDN:CAA34655.1; PID:G32382
R:Kongswan, K.; Webb, E.; Housiaux, P.; Adams, J.M.
EMBO J. 7, 2131-2138, 1988
A:Title: Expression of multiple homeobox genes within diverse mammalian haemopoietic li
A:Reference number: S00987; MUID:88329001; PMID:2901346
A:Accession: S00989
A:Molecule type: mRNA
A:Residues: 143-202 <KON>
A:Cross-references: EMBL:X14571; NID:G32034; PIDN:CAA32709.1; PID:G930065
R:Boncinelli, E.; Acampora, D.; Pannese, M.; d'Esposito, M.; Somma, R.; Gaudino, G.; St
Genome 31, 745-756, 1989
A:Title: Organization of human class I homeobox genes.
A:Reference number: S15036; MUID:90215256; PMID:2576652
A:Accession: S15549
A:Molecule type: DNA
A:Residues: 143-208 <BON>
R:Vielle-Grosjean, I.; Huber, P.
J. Biol. Chem. 270, 4544-4550, 1995
A:Title: Transcription factor GATA-1 regulates human HOXB2 gene expression in erythroid
A:Reference number: A56093; MUID:95181447; PMID:7876223
A:Accession: A56093
A:Molecule type: DNA
A:Residues: 1-42 <VIZ>
A:Cross-references: GB:X78978; NID:G475199; PIDN:CAA55581.1; PID:G475200
R:Giampolo, A.; Acampora, D.; Zappavigna, V.; Pannese, M.; D'Esposito, M.; Care, A.; F
Differentiation 40, 191-197, 1989
A:Title: Differential expression of human HOX-2 genes along the anterior-posterior axis

A:Reference number: A37042; MUID:89378558; PMID:2570724
A:Accession: E37042
A:Molecule type: DNA
A:Residues: 132-135, RRL, 139-208 <GIA>
A:Cross-references: GB:X16176; NID:G32378; PIDN:CAA34298.1; PID:g930069
C:Genetics:
A:Gene: GDB:HOXB2
A:Cross-references: GDB:120665; OMIM:142967
A:Map position: 17q21.3-17q21.3
A:Introns: 131/1
C:Superfamily: homeotic protein Hox B2; homeobox homology
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation
F:76-96/Region: proline-rich
F:144-200/Domain: homeobox homology <HOX>

Query Match 11.9%; Score 115; DB 1; Length 356;
Best Local Similarity 24.7%; Pred. No. 0.17;
Matches 56; Conservative 15; Mismatches 68; Indels 88; Gaps 11;

QY 5 PRS-LRGDAPA-----PTPCVPAECFDLLVRHCVACGLLRTTRP-----KPXA 47
DB 66 PRSQKAEDGALPPPPPPPLPA-----APPAEFPWMKKSAKPSQ 109

QY 48 GASSAPRTRALQPSVGVGAGEAALPLPG-----LL-----FG 81
DB 110 SATSPSPASAVPASGVGSPADGLGPAAGGGARLRATYNTQLLEKEPFFNKYLC 169

QY 82 APALLGLALVLALVGLVSW---RRQRRLRGASSAEAPDGKDAPPLDKVI-----I 133
DB 170 RPRVEIALLDLTERQVAVWFQNRMKHKRQTHREPPDGEPACPGALEDICDPAEPA 229

QY 134 LSPGISDATAPW-----PP-----PG-----EDGTTTPG 159
DB 230 ASPGSPSARRAAWEACCHPEVVPVVGALSADPLAVRLGAGASSPG 276

RESULT 6
T46289
Hypothetical protein DKFZp344l010.1 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
C:Accession: T46289
R:Duisterhoef, A.; Lauber, J.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, January 2000
A:Reference number: 223035
A:Accession: T46289
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-862 <AAA>
A:Cross-references: EMBL:AL137579
A:Experimental source: adult testis; clone DKFZp344l010
C:Genetics:
A:Note: DKFZp344l010.1

Query Match 11.9%; Score 114.5; DB 2; Length 862;
Best Local Similarity 27.0%; Pred. No. 0.43;
Matches 60; Conservative 16; Mismatches 75; Indels 71; Gaps 11;

QY 10 GRDAP--APTFCVPAECFDLLVRHCVACGLLRTTRPKXA---GASSAPRTRALQPOES 63
DB 328 GDPAPPASPAPPASAF-----PPRTTPQAIISPRGTSFASPAALDISEP 373

QY 64 -----VGAGAGEA-ALPLPOLLFG---APALLGLALVLALVGLVSWRRQR 107
DB 374 LAVSVPPAVLELLGAGGAPASATPTPALSPPGSLRPHLIPLLIRGAEAAPLTDACQEMCS 433

QY 108 RLRGASSAEAPDGKDAPELDKVIILSPGISDATAPAMPPGDEP----- 153
DB 434 KLRGAQGLGPDMSPLPPP---PLSLRPG-----GAP---PPPPKPNRLMALALERAQQ 485

QY 154 -----GTTTPPGHVSVPV---ATELGSTELVTTKTAG 182
DB 486 VAEQSQEQECGCTTPASQSPHRSLSLEVGEPLGTSGSGPP 527

A:Reference number: A37042; MUID:89378558; PMID:2570724
A:Accession: E37042
A:Molecule type: DNA
A:Residues: 132-135, RRL, 139-208 <GIA>
A:Cross-references: GB:X16176; NID:G32378; PIDN:CAA34298.1; PID:g930069
C:Genetics:
A:Gene: GDB:HOXB2
A:Cross-references: GDB:120665; OMIM:142967
A:Map position: 17q21.3-17q21.3
A:Introns: 131/1
C:Superfamily: homeotic protein Hox B2; homeobox homology
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation
F:76-96/Region: proline-rich
F:144-200/Domain: homeobox homology <HOX>

Query Match 11.9%; Score 115; DB 1; Length 356;
Best Local Similarity 24.7%; Pred. No. 0.17;
Matches 56; Conservative 15; Mismatches 68; Indels 88; Gaps 11;

QY 5 PRS-LRGDAPA-----PTPCVPAECFDLLVRHCVACGLLRTTRP-----KPXA 47
DB 66 PRSQKAEDGALPPPPPPPLPA-----APPAEFPWMKKSAKPSQ 109

QY 48 GASSAPRTRALQPSVGVGAGEAALPLPG-----LL-----FG 81
DB 110 SATSPSPASAVPASGVGSPADGLGPAAGGGARLRATYNTQLLEKEPFFNKYLC 169

QY 82 APALLGLALVLALVGLVSW---RRQRRLRGASSAEAPDGKDAPPLDKVI-----I 133
DB 170 RPRVEIALLDLTERQVAVWFQNRMKHKRQTHREPPDGEPACPGALEDICDPAEPA 229

QY 134 LSPGISDATAPW-----PP-----PG-----EDGTTTPG 159
DB 230 ASPGSPSARRAAWEACCHPEVVPVVGALSADPLAVRLGAGASSPG 276

RESULT 6
T46289
Hypothetical protein DKFZp344l010.1 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
C:Accession: T46289
R:Duisterhoef, A.; Lauber, J.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, January 2000
A:Reference number: 223035
A:Accession: T46289
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-862 <AAA>
A:Cross-references: EMBL:AL137579
A:Experimental source: adult testis; clone DKFZp344l010
C:Genetics:
A:Note: DKFZp344l010.1

Query Match 11.9%; Score 114.5; DB 2; Length 862;
Best Local Similarity 27.0%; Pred. No. 0.43;
Matches 60; Conservative 16; Mismatches 75; Indels 71; Gaps 11;

QY 10 GRDAP--APTFCVPAECFDLLVRHCVACGLLRTTRPKXA---GASSAPRTRALQPOES 63
DB 328 GDPAPPASPAPPASAF-----PPRTTPQAIISPRGTSFASPAALDISEP 373

QY 64 -----VGAGAGEA-ALPLPOLLFG---APALLGLALVLALVGLVSWRRQR 107
DB 374 LAVSVPPAVLELLGAGGAPASATPTPALSPPGSLRPHLIPLLIRGAEAAPLTDACQEMCS 433

QY 108 RLRGASSAEAPDGKDAPELDKVIILSPGISDATAPAMPPGDEP----- 153
DB 434 KLRGAQGLGPDMSPLPPP---PLSLRPG-----GAP---PPPPKPNRLMALALERAQQ 485

QY 154 -----GTTTPPGHVSVPV---ATELGSTELVTTKTAG 182
DB 486 VAEQSQEQECGCTTPASQSPHRSLSLEVGEPLGTSGSGPP 527

RESULT 7
S72273
actin-depolymerizing protein N-WASP, brain - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 23-Apr-1998 #sequence_revision 01-May-1998 #text_change 05-Nov-1999
C:Accession: S72273
R:Miki, H.; Miura, K.; Takenawa, T.
EMBO J. 15, 5326-5335, 1996
A:Title: N-WASP, a novel actin-depolymerizing protein, regulates the cortical cytoskeleton
A:Reference number: S72273; MUID:97050838; PMID:8895577
A:Accession: S72273
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-505 <MIX>
A:Cross-references: EMBL:D67066; NID:g1644231; PIDN:BAAL1082.1; PID:di011742; PID:gl644
A:Experimental source: brain

Query Match 11.0%; Score 106.5; DB 2; Length 505;
Best Local Similarity 23.3%; Pred. No. 1;
Matches 41; Conservative 4; Mismatches 44; Indels 87; Gaps 6;

QY 5 PRSLRGDAP-----APTFCVPAECFDLLVRHCVACGLLRTTRPKPKXAGASSAPRTRAL 58
DB 301 PPPARGRGARPPPPPSRAPTAAPP-----PPPSRPGVGAPPPPPNRMV 343

QY 59 QPQSVGVGAGEAALPLPGLLFGAPALLGLALVLALVGLVSWRRQRRLRGASSAEAP 118
DB 344 PP-----PUPAL-----PSSAP 355

QY 119 DQDKDAPELDKVIILSPGISDATAPAMPPGDEGTTTP-----GHSVVPVA 166
DB 356 SQPPPPPPPL-----SVSGSVAPPPPPPPPPPPPPGLPSDGDQVPTPA 403

RESULT 8
B35098
MHC class III histocompatibility antigen HLA-B-associated protein 2 [imported] - human
C:Species: Homo sapiens (man)
C:Date: 10-Aug-1990 #sequence_revision 06-Nov-1992 #text_change 24-Aug-2001
C:Accession: B35098
R:Banerji, J.; Sands, J.; Strominger, J.L.; Spies, T.
Proc. Natl. Acad. Sci. U.S.A. 87, 2374-2378, 1990
A:Title: A gene pair from the human major histocompatibility complex encodes large protein
A:Reference number: A35098; MUID:90192810; PMID:2156268
A:Accession: B35098
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-2142 <BAN>
A:Cross-references: GB:M33509; NID:g179338; PIDN:AAA35585.1; PID:g179339; GB:M31293
A:Note: the authors translated the codon AGT for residue 97 as Gly
C:Superfamily: collagen alpha 1(IV) chain

Query Match 10.9%; Score 105.5; DB 2; Length 2142;
Best Local Similarity 24.9%; Pred. No. 4.6;
Matches 46; Conservative 16; Mismatches 48; Indels 75; Gaps 10;

QY 14 PAPTFCVPAECFDLLVRHCVACGLLRTTRPKXAGASSAPRTRALQPOESVGAGAGEAL 73
DB 506 PAPPAPAPVPE-----LPAPPAPPP-----ASAPTET--EPPEPAQAPPAQST- 546

QY 74 PLPGLLFGAPALLGLALVLALVGLVSWRRQRRLRGASSAEAPDG-----D 121
DB 547 FTGVA-AAPTLV-----GGSTSSSSSGSFEASPVPEQLPS 583

QY 122 KDAPELDKVIILSPGISDATAPAMPPGDEGTTTPGHSVVPVVPATELGSTELVTTKTAG 181
DB 584 KEGPEPPEV-----PPP-----TTPPVKVEPKGDGIGTPRPPSQGLG 623

QY 182 -PEQQ 185
DB 624 YPKYQ 628

```
RESULT 9
CW17R protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 05-Nov-1999
R/Schmitt-Wrede, H.P.; Wrehle, C.; Qiao, Z.D.; Heischkamp, H.; Bente, W.P.M.; Wunderli
submitted to the EMBL Data Library, March 1995
A:Description: Testosterone-induced immunosuppression of Plasmodium chabaudi malaria: di
A:Reference number: S52735
A:Accession: S52735
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-548 <SCH>
A:Cross-references: EMBL:X85802; NID:g1332610; PID:CAA59797.1; PID:g758299

Query Match 10.7%; Score 103.5; DB 2; Length 548;
Best Local Similarity 22.9%; Pred. No. 1.8;
Matches 43; Conservative 14; Mismatches 52; Indels 79; Gaps 8;

QY 5 PRSLGRDAPPTPCVPACFCDLLVHVCAGLLRTPPKPKXAGASSPAPRTALQPOES- 63
DB 326 PASVGSTGSPATPLASA-----PRPAAPASNPFPFSLMSTTQSR 365

QY 64 ---VGAGAGAAALPLGALLFGAPALLGLALVLALVGLVSWRRQRRLRGASSAEAPDG 120
DB 366 PPWNNSQPSNR-PYGMHCGGPGGPG-----GG 393

QY 121 DXDAPEPLDKVILSLSGIS-----DATAPAW---PPGDEGTTPPGHVSVPVP 165
DB 394 PHSFPHL-----PSLTGGHGHQPMHNPNGPPPMQPPPPPMNQGHPPHPPGHGPP 446

QY 166 ATE-LGST 172
DB 447 MDQLGST 454

RESULT 10
EDBEF6
155K transcription activator - equine herpesvirus 1 (strain Ab4p)
C:Species: equine herpesvirus 1
A:Note: host Equus caballus (domestic horse)
C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 16-Jul-1999
C:Accession: A36802
R:Teiford, E.A.R.; Watson, M.S.; McBride, K.; Davison, A.J.
submitted to GenBank, March 1992
A:Description: The DNA sequence of equine herpesvirus-1.
A:Reference number: A36805
A:Accession: A36802
A:Molecule type: DNA
A:Residues: 1-1487 <TEL>
A:Cross-references: GB:M86664; NID:g330791; PID:AA02499.1; PID:g330855
R:Teiford, E.A.R.; Watson, M.S.; McBride, K.; Davison, A.J.
Virology 189, 304-316, 1992
A:Title: The DNA sequence of equine herpesvirus-1.
A:Reference number: A41831; MUID:92295566; PMID:1318606
A:Contents: annotation; possible protein-coding frames
A:Note: neither amino acid nor nucleotide sequence is given
C:Genetics:
A:Gens: 64
C:Superfamily: herpesvirus immediate-early protein IE175
C:Keywords: DNA binding; early protein; transcription regulation

Query Match 10.7%; Score 103.5; DB 1; Length 1487;
Best Local Similarity 28.7%; Pred. No. 4.6;
Matches 45; Conservative 11; Mismatches 62; Indels 39; Gaps 8;

QY 12 DAPATPCV---PAECFDLLVHVCAGLLRTPPKPKXAGASSPAPRTALQPOESVGAGAG 69
DB 57 DAPLSTPAVVPPP-----SPAPEPGKAKRSPSAAGSGGPTTAAAA 100

QY 70 EAALPLGALLFGAPALLGLALVLALVGLVSWRRQRRLRGASSAEAPDGKDAPEPLD 129
DB 101 QPASAP-----SPA-PGLAAMLKXVHSSVAPGNR----RATGSSPGGGDAADPVALD 150

QY 130 KVIILSPGISA-TAPAWPPPGEDDPTTPPGHVSVPVP 165
DB 151 -----SDTETCPGSPQ-PFPSSASPGGSPAP 177

RESULT 11
EDBEE1
immediate-early protein - equine herpesvirus 1
C:Species: equine herpesvirus 1
C:Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 16-Jul-1999
C:Accession: A33764
R:Grundy, F.J.; Baumann, R.P.; O'Callaghan, D.J.
Virology 172, 223-236, 1989
A:Title: DNA sequence and comparative analyses of the equine herpesvirus type 1 immedia
A:Reference number: A33764; MUID:89370304; PMID:12549711
A:Accession: A33764
A:Molecule type: DNA
A:Residues: 1-1487 <GRU>
A:Cross-references: GB:J04366; NID:g330910; PID:AAA46089.1; PID:g330911
C:Superfamily: herpesvirus immediate-early protein IE175
C:Keywords: DNA binding; early protein; transcription regulation

Query Match 10.6%; Score 102.5; DB 1; Length 1487;
Best Local Similarity 28.7%; Pred. No. 5.5;
Matches 45; Conservative 11; Mismatches 62; Indels 39; Gaps 8;

QY 12 DAPATPCV---PAECFDLLVHVCAGLLRTPPKPKXAGASSPAPRTALQPOESVGAGAG 69
DB 57 DAPLSTPAVVPPP-----SPAPEPGKAKRSPSAAGSGGPTTAAAA 100

QY 70 EAALPLGALLFGAPALLGLALVLALVGLVSWRRQRRLRGASSAEAPDGKDAPEPLD 129
DB 101 QPASAP-----SPA-PGLAAMLKXVHSSVAPGNR----RATGSSPGGGDAADPVALD 150

QY 130 KVIILSPGISA-TAPAWPPPGEDDPTTPPGHVSVPVP 165
DB 151 -----SDTETCPGSPQ-PFPSSASPGGSPAP 177

RESULT 12
EDBS22
immediate-early protein IER2.9 - bovine herpesvirus 1 (strain K22)
N:Alternate names: early protein ER2.6; p135 protein
C:Species: bovine herpesvirus 1
C:Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 17-Mar-2000
C:Accession: A38209
R:Wirth, U.V.; Fraefel, C.; Vogt, B.; Vlcek, C.; Paces, V.; Schwyzer, M.
J. Virol. 66, 2763-2772, 1992
A:Title: Immediate-early RNA 2.9 and early RNA 2.6 of bovine herpesvirus 1 are 3' coter
A:Reference number: A38209; MUID:92219360; PMID:1313901
A:Accession: A38209
A:Molecule type: DNA
A:Residues: 1-676 <WIR>
A:Cross-references: GB:M84464; NID:g330767; PID:AAA46061.1; PID:g330768
C:Superfamily: herpesvirus immediate-early protein IE110; RING finger homology
C:Keywords: DNA binding; immediate-early protein; transcription regulation; zinc finger
F:9-57/Domain: RING finger homology <RNG>
F:13-51/Region: zinc finger C3HC4 motif
F:284-331/Region: acidic

Query Match 10.6%; Score 102; DB 1; Length 676;
Best Local Similarity 29.9%; Pred. No. 2.9;
Matches 60; Conservative 14; Mismatches 83; Indels 44; Gaps 10;

QY 7 SLRGDAPATPCVPACFCDLLVHVCAG-----GLLTPR-----PKPX 46
DB 353 STRGQTPAVQAPRS-----LARRPCGRAAAVAPSSRSRGRDRPLPAAPRAAPAAQ 408
QY 47 AGASSPAPRTALQPOESVGAGAGAAALPLPLGLFGAPALLGLALVLALVGLV-----LVSWR 103
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```
QY 70 EAALPLGALLFGAPALLGLALVLALVGLVSWRRQRRLRGASSAEAPDGKDAPEPLD 129
DB 101 QPASAP-----SPA-PGLAAMLKXVHSSVAPGNR----RATGSSPGGGDAADPVALD 150

QY 130 KVIILSPGISA-TAPAWPPPGEDDPTTPPGHVSVPVP 165
DB 151 -----SDTETCPGSPQ-PFPSSASPGGSPAP 177

RESULT 11
EDBEE1
immediate-early protein - equine herpesvirus 1
C:Species: equine herpesvirus 1
C:Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 16-Jul-1999
C:Accession: A33764
R:Grundy, F.J.; Baumann, R.P.; O'Callaghan, D.J.
Virology 172, 223-236, 1989
A:Title: DNA sequence and comparative analyses of the equine herpesvirus type 1 immedia
A:Reference number: A33764; MUID:89370304; PMID:12549711
A:Accession: A33764
A:Molecule type: DNA
A:Residues: 1-1487 <GRU>
A:Cross-references: GB:J04366; NID:g330910; PID:AAA46089.1; PID:g330911
C:Superfamily: herpesvirus immediate-early protein IE175
C:Keywords: DNA binding; early protein; transcription regulation

Query Match 10.6%; Score 102.5; DB 1; Length 1487;
Best Local Similarity 28.7%; Pred. No. 5.5;
Matches 45; Conservative 11; Mismatches 62; Indels 39; Gaps 8;

QY 12 DAPATPCV---PAECFDLLVHVCAGLLRTPPKPKXAGASSPAPRTALQPOESVGAGAG 69
DB 57 DAPLSTPAVVPPP-----SPAPEPGKAKRSPSAAGSGGPTTAAAA 100

QY 70 EAALPLGALLFGAPALLGLALVLALVGLVSWRRQRRLRGASSAEAPDGKDAPEPLD 129
DB 101 QPASAP-----SPA-PGLAAMLKXVHSSVAPGNR----RATGSSPGGGDAADPVALD 150

QY 130 KVIILSPGISA-TAPAWPPPGEDDPTTPPGHVSVPVP 165
DB 151 -----SDTETCPGSPQ-PFPSSASPGGSPAP 177

RESULT 12
EDBS22
immediate-early protein IER2.9 - bovine herpesvirus 1 (strain K22)
N:Alternate names: early protein ER2.6; p135 protein
C:Species: bovine herpesvirus 1
C:Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 17-Mar-2000
C:Accession: A38209
R:Wirth, U.V.; Fraefel, C.; Vogt, B.; Vlcek, C.; Paces, V.; Schwyzer, M.
J. Virol. 66, 2763-2772, 1992
A:Title: Immediate-early RNA 2.9 and early RNA 2.6 of bovine herpesvirus 1 are 3' coter
A:Reference number: A38209; MUID:92219360; PMID:1313901
A:Accession: A38209
A:Molecule type: DNA
A:Residues: 1-676 <WIR>
A:Cross-references: GB:M84464; NID:g330767; PID:AAA46061.1; PID:g330768
C:Superfamily: herpesvirus immediate-early protein IE110; RING finger homology
C:Keywords: DNA binding; immediate-early protein; transcription regulation; zinc finger
F:9-57/Domain: RING finger homology <RNG>
F:13-51/Region: zinc finger C3HC4 motif
F:284-331/Region: acidic

Query Match 10.6%; Score 102; DB 1; Length 676;
Best Local Similarity 29.9%; Pred. No. 2.9;
Matches 60; Conservative 14; Mismatches 83; Indels 44; Gaps 10;

QY 7 SLRGDAPATPCVPACFCDLLVHVCAG-----GLLTPR-----PKPX 46
DB 353 STRGQTPAVQAPRS-----LARRPCGRAAAVAPSSRSRGRDRPLPAAPRAAPAAQ 408
QY 47 AGASSPAPRTALQPOESVGAGAGAAALPLPLGLFGAPALLGLALVLALVGLV-----LVSWR 103
```

Db 409 ARACSEPR-----EGRGAGLVNAGTAGWGSSEGRERAKLLGAGPRVQARR 463
QY 104 RRQRKL-RCASAEAPDGDQKDAPELDKVIILSPGIGSDATA-PAWPPPGDGGTTPPGHS 161
Db 464 RRRTLDRAFTAPAP---APAPAPISTMIDL---ANAPAPADPAPAAALGPALAGAQ 517
QY 162 VVPVATGLSTELVTTKTAGP 182
Db 518 IGTPA-----AANAATAAAAP 534

RESULT 13
T42761
Bassoon protein - rat
N:Alternate names: brain-specific synapse-associated protein
C:Species: Rattus norvegicus (Norway rat)
C>Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 21-Jul-2000
C:Accession: T42761
R:Dieck, S.; Sammarti-Vila, L.; Langnaese, K.; Richter, K.; Kindler, S.; Soyke, A.; Wex, J. Cell Biol. 142, 499-509, 1998
A:Title: Bassoon, a novel zinc-finger CAG/Glutamine-repeat protein selectively localized
A:Reference number: 222249; MUID:98345363; PMID:9679147
A:Accession: T42761
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-3938 <DIE>
A:Cross-references: EMBL:Y16563; NID:G3413503; PIDN:CAA76287.1; PID:G3413504
A:Experimental source: strain Sprague Dawley; brain
C:Function:
A:Description: may be involved in cytomatrix organization at the site of neurotransmitter
A>Note: component of the presynaptic cytoskeleton
C:Keywords: coiled coil; zinc finger

Query Match 10.6%; Score 102; DB 2; Length 3938;
Best Local Similarity 24.6%; Pred. No. 15;
Matches 50; Conservative 14; Mismatches 71; Indels 68; Gaps 9;
QY 4 GPR---SLGRDAPATPCVPAECFDLLVRHCVACGLLTPRPKEXAGASPAP-----R 55
Db 272 GPRQAEARATSPVPGTQAT-----APPEVGRVSPQPLSTKP 309
QY 56 TALQPOESVAGAGEAALPLP-----GLLFGAPALGLALVLALVLGLVS 101
Db 310 STAEPPPPAGEAGKATVPSGLNAEQTQGLTGKFLGLGSL---LTQASTLMSVQ 366
QY 102 WRRRRLRGASAEAPDGDQKDAPELDKVIILSPGIGSDATAWPPP---GEDPGTTPP 158
Db 367 -----EADTQGGPSPSKGPP---KIV-----FSDASKEAGPRPPGGGPGTTPG 408
QY 159 GHSVVPVATGLSTELVTTKTAG 181
Db 409 AKTEPGRTGPGSGPGALAKTGG 431

RESULT 14
B56708
extracellular signal-regulated kinase 5 - human
C:Species: Homo sapiens (man)
C>Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 24-Sep-1999
C:Accession: B56708
R:Zhou, G.; Bao, Z.Q.; Dixon, J.E.
J. Biol. Chem. 270, 12665-12669, 1995
A:Title: Components of a new human protein kinase signal transduction pathway.
A:Reference number: A56708; MUID:95279403; PMID:7759517
A:Accession: B56708
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-815 <ZHO>
A:Cross-references: GB:U25278; NID:G837260; PIDN:AAA81381.1; PID:G837261
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolc
C:Keywords: Atp
F:52-315/Domain: protein kinase homology <KIN>

F:60-68/Region: protein kinase ATP-binding motif
Query Match 10.5%; Score 101.5; DB 2; Length 815;
Best Local Similarity 23.08; Pred. No. 3.7;
Matches 58; Conservative 19; Mismatches 76; Indels 99; Gaps 11;
QY 14 PAPTPCV-PA-ECFDLLV-----RHCVACGLLTPPK-----P 45
Db 435 PAPPPCPGAPDITDLTLQPPFPVSBPAPPKDGAISDNTKAALKAAALKSLRSRLRDGP 494
QY 46 XAGASSPAPRTALQPOE-----SVGAGAGAAALP 74
Db 495 SAPLEAPEPRKPVTAQQRERERERERERERERERERERERERERERERERERERER 554
QY 75 LPGLLFGAPALLGLALVLVLV-----LVSWRRQRRLRGA-SSAEAP----- 118
Db 555 LAG-----LVLSNDRSLLETRMARPAAPALTSVPAPAPATPTPTTP 598
QY 119 -DGDKDAPELDKVIILSPGIGSDATA-----PAWPPPGDGGTTPPGHSVVPVATE--LG 170
Db 599 VQTPSPPPGGLAQGTGPOQOSAGSTSGFVQPCACPPGPPAPHTGTGPPGPIPVAPPQIAT 658
QY 171 STELVVTKTAGP 182
Db 659 STSLAAQSLVP 670

RESULT 15
S55659
tegument protein 64 - equine herpesvirus 2
C:Species: equine herpesvirus 2
C>Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 08-Oct-1999
C:Accession: S55659
R:Wellford, E.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.
J. Mol. Biol. 249, 520-528, 1995
A:Title: The DNA sequence of equine herpesvirus 2.
A:Reference number: S55594; MUID:95302501; PMID:7783207
A:Accession: S55659
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-3436 <TEL>
A:Cross-references: GB:U20824; NID:G695172; PIDN:AA13852.1; PID:G695237
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1995

Query Match 10.5%; Score 101.5; DB 2; Length 3436;
Best Local Similarity 26.6%; Pred. No. 14;
Matches 54; Conservative 15; Mismatches 67; Indels 67; Gaps 11;
QY 2 RRGPSRLRGD-----APAP-----TPCVPACFDLLVRHCVACGLLTPRPKEXAGASP 52
Db 3178 RLGERGRER 3218
QY 53 APRTALQPOESVAGAGEAALPLPGLLFGAPALGLALVLALVLGLVSWRRQ----- 106
Db 3219 A-----RDRDILGGAGSREKVSER--GRPRVQLSRSPKPRPAASQVQPREVGFSPG 3271
QY 107 RELRGASAEAPDGDQKDAPELDKVIILSP-----GISDATAPWPPP 149
Db 3272 RARRGGSTAHP-----PE-TDTADYIEPPKSGVAGSGPPEKXQQQAAAEAPA-PRE 3323
QY 150 GEDPGTTPPGHSVVPVATGLST 172
Db 3324 GEGAAQAPGEGTPEPAS-IGKT 3345

Search completed: February 5, 2004, 18:01:28
Job time : 15.875 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 5, 2004, 17:49:49 ; Search time 10.2778 Seconds
(without alignments)
846.481 Million cell updates/sec

Title: US-10-045-574B-27

Perfect score: 966

Sequence: 1 NRRGPRSLRGDAPAPTCV.....ATELGSTELVTIKTAGPEQQ 185

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	954.5	98.8	184	1 T13C_HUMAN	Q96R33 homo sapien
2	411	42.5	175	1 T13C_MOUSE	Q9d8d0 mus musculus
3	118.5	12.3	439	1 XP2_XENLA	P17437 xenopus lae
4	116	12.0	676	1 ICP0_HSVBJ	P29128 bovine herp
5	115	11.9	356	1 HXB2_HUMAN	P14652 homo sapien
6	110.5	11.4	1186	1 HCN4_MOUSE	O70507 mus musculus
7	110	11.4	1083	1 T2D3_HUMAN	O00268 homo sapien
8	106.5	11.0	505	1 WASL_BOVIN	Q95107 bos taurus
9	106.5	11.0	1198	1 HCN4_RAT	Q91k47 rattus norv
10	105.5	10.9	2142	1 BAT2_HUMAN	P48634 homo sapien
11	103.5	10.7	625	1 DUS8_HUMAN	Q13202 homo sapien
12	103.5	10.7	1487	1 ICP4_HSVB	P28925 equine herp
13	103	10.7	1003	1 MB06_HUMAN	Q96dn6 homo sapien
14	102.5	10.6	1487	1 ICP4_HSVB	P17473 equine herp
15	102	10.6	676	1 ICP0_HSVB	P29836 bovine herp
16	101.5	10.5	815	1 MK07_HUMAN	Q13164 homo sapien
17	101	10.5	915	1 A180_RAT	Q05140 rattus norv
18	100.5	10.4	725	1 AREA_PENCH	Q01582 penicillium
19	99	10.2	503	1 IREF7_HUMAN	Q92985 homo sapien
20	98.5	10.2	323	1 DBP_HUMAN	Q10586 homo sapien
21	98.5	10.2	1175	1 HCN4_RABIT	Q9tcv66 oryctolagus
22	97.5	10.1	317	1 YQ35_CAEEL	Q09456 caenorhabdi
23	97.5	10.1	722	1 Z219_HUMAN	Q9p2y4 homo sapien
24	97	10.0	520	1 RXRB_MOUSE	P28704 mus musculus
25	96.5	10.0	1509	1 GSRI_HUMAN	Q9zpm4 homo sapien
26	95	9.8	129	1 FN14_HUMAN	Q9np84 homo sapien
27	95	9.8	316	1 CDNC_HUMAN	P49918 homo sapien
28	95	9.8	901	1 A180_MOUSE	Q61548 mus musculus
29	94.5	9.8	185	1 TR17_MOUSE	O88472 mus musculus
30	94.5	9.8	551	1 PODX_RABIT	Q28645 oryctolagus
31	94.5	9.8	1229	1 P121_HUMAN	Q9y2n3 homo sapien
32	94	9.7	316	1 CC07_CAEEL	P18832 caenorhabdi
33	94	9.7	625	1 NIPA_AOBER	P30667 azospirillum

ALIGNMENTS

```

RESULT 1
T13C_HUMAN
ID T13C_HUMAN STANDARD; PRT; 184 AA.
AC Q96R33;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 13C (B cell-
DE activating factor receptor) (BAFF receptor) (BAFF-R) (BLyS receptor
DE 3).
GN TNFRSF13C OR BAFFR OR BR3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RX TISSUE=B-cell lymphoma;
RX MEDLINE=21442025; PubMed=11509692;
RA Thompson J.S., Bixler S.A., Qian F., Vora K., Scott M.L.,
RA Cachero T.G., Hession C., Schneider P., Sizing I.D., Mullen C.,
RA Strauch K., Zafari M., Benjamin C.D., Tschopp J., Browning J.L.,
RA Ambrose C.;
RA "BAFF-R, a newly identified TNF receptor that specifically interacts
RT with BAFF.";
RT Science 293:2108-2111(2001).
RN [2]
RP FUNCTION.
RX MEDLINE=21475520; PubMed=11591325;
RA Yan M., Brady J.R., Chan B., Lee W.P., Hsu B., Harless S.M.,
RA Cancro M.P., Grewal I.S., Dixit V.M.;
RA "Identification of a novel receptor for B lymphocyte stimulator that
RT is mutated in a mouse strain with severe B cell deficiency.";
RX Curr. Biol. 11:1547-1552(2001).
CC -!- FUNCTION: B-cell receptor specific for TNFSF13B/TALL1/BAFF/BLyS.
CC Promotes the survival of mature B-cells and the B-cell response.
CC -!- SUBCELLULAR LOCATION: Type III membrane protein (Probable).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q96R33-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q96R33-2; Sequence=VSP_006505;
CC Note=No experimental confirmation available;
CC -!- TISSUE SPECIFICITY: Highly expressed in spleen and lymph node, and
CC in resting B-cells. Detected at lower levels in activated B-cells,
CC resting CD4+ T-cells, in thymus and peripheral blood leukocytes.
CC -!- SIMILARITY: Contains 1 TNFR-Cys repeat.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.ebi.ac.uk/announcement/
CC or send an email to license@ebi.ac.uk).
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Q9GKY7 oryctolagus
O18964 bos taurus
P20908 homo sapien
P50284 mus musculus
Q92949 homo sapien
O75154 homo sapien
Q9Y566 homo sapien
P50551 canis famil
O60309 homo sapien
Q15735 homo sapien
Q02223 homo sapien
P08353 herpes simp

34 94 9.7 694 1 JPH2_RABIT
35 94 9.7 1324 1 SYJ1_BOVIN
36 94 9.7 1838 1 CAL5_HUMAN
37 93.5 9.7 415 1 TNR3_MOUSE
38 93.5 9.7 421 1 FXJ1_HUMAN
39 93.5 9.7 756 1 EFER_HUMAN
40 93.5 9.7 2161 1 SHK1_HUMAN
41 93 9.6 384 1 VASP_CANFA
42 93 9.6 870 1 Y563_HUMAN
43 93 9.6 1006 1 P5PA_HUMAN
44 92.5 9.6 184 1 TR17_HUMAN
45 92.5 9.6 263 1 ICP3_HSVIF

```

CC EMBL; AF373846; AAK91826.1; -.
DR PDB; 1MV; 30-OCT-02
DR Genew; HGNC:17755; TNFRSF13C.
DR MIM; 606269; -.
DR InterPro; IPRO01368; TNFR-C6.
DR PROSITE; P80652; TNFR_NGFR_1; FALSE NEG.
DR PROSITE; P80650; TNFR_NGFR_2; FALSE NEG.
KW Receptor; Immune response; Signal-anchor; Transmembrane;
KW Alternative splicing; 3D-structure.
FT DOMAIN 1 78 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 79 99 SIGNAL-ANCHOR
FT DOMAIN 100 184 CYTOPLASMIC (POTENTIAL).
FT REPEAT 18 35 TNFR-CYS (PARTIAL).
FT DISULFID 19 32 BY SIMILARITY.
FT DISULFID 24 35 BY SIMILARITY.
FT VARSPLIC 143 143 P -> PA (in isoform 2).
FT SEQUENCE 184 AA; 18863 MW; F28FB9809A27138 CRC64;
Query Match 98.8%; Score 954.5; DB 1; Length 184;
Best Local Similarity 99.5%; Pred. No. 4.5e-58;
Matches 184; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 MRGSPSLRGDRAPATPCVPAECFDLLVRHCACGLLRTPRPKPKXGASSPAPRTALQP 60
Db 1 MRGSPSLRGDRAPATPCVPAECFDLLVRHCACGLLRTPRPKPKXGASSPAPRTALQP 59
QY 61 QESVGAGAGEAALPLFGLLFGAPALLGLALVLVGLVSWRRQRRLRGASSAEAPDG 120
Db 60 QESVGAGAGEAALPLFGLLFGAPALLGLALVLVGLVSWRRQRRLRGASSAEAPDG 119
QY 121 DKDAPDLKVIILSPGISDATAPAPPPGDPGTPPHSHVVPVPAELGSLTVTKTA 180
Db 120 DKDAPDLKVIILSPGISDATAPAPPPGDPGTPPHSHVVPVPAELGSLTVTKTA 179
QY 181 GPEQQ 185
Db 180 GPEQQ 184
RESULT 2
T13C MOUSE STANDARD; PRT; 175 AA.
AC Q9B8D0;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 13C (B cell-
DE activating factor receptor) (BAFF receptor) (BAFF-R) (Blys receptor
DE 3) (B-cell maturation defect).
DE TNFRSF13C OR BAFFR OR BCMD OR BR3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_taxid=10090;
[1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC STRAIN=BALB/c; TISSUE=B-cell lymphoma;
RX MEDLINE=21442025; PubMed=11509692;
RA Thompson J.S., Bixler S.A., Qian F., Vora K., Scott M.L.,
RA Cachero T.G., Hession C., Schneider P., Sizing I.D., Mullen C.,
RA Strauch K., Zafari M., Benjamin C.D., Tschopp J., Browning J.L.,
RA Ambrose C.;
RA "BAFF-R, a newly identified TNF receptor that specifically interacts
RT with BAFF."
RL Science 293:2108-2111(2001).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND DISEASE.
RC STRAIN=A/J;75520; PubMed=11591325;
RX MEDLINE=21475520;
RA Yan M., Brady J.R., Chan B., Lee W.P., Hsu B., Harless S.M.,

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RA Canro M.P., Grewal I.S., Dixit V.M.;
RT "Identification of a novel receptor for B lymphocyte stimulator that
RT is mutated in a mouse strain with severe B cell deficiency."
RL Curr. Biol. 11:1547-1552(2001).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC STRAIN=C57BL/6J; TISSUE=Small intestine;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saio T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gusninch S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., King B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
RN [4]
RP FUNCTION.
RX MEDLINE=21614654; PubMed=11747827;
RA Harless S.M., Lentz V.M., Sah A.P., Hsu B.L., Clise-Dwyer K.,
RA Hilbert D.M., Hayes C.E., Canro M.P.;
RT "Competition for Blys-mediated signaling through Bcmd/BR3 regulates
RT peripheral B lymphocyte numbers."
RL Curr. Biol. 11:1386-1389(2001).
CC -!- FUNCTION: B-cell receptor specific for TNFSF13B/TALL1/BAFF/Blys.
CC Promotes the survival of mature B-cells and the B-cell response.
CC -!- SUBCELLULAR LOCATION: Type III membrane protein (Probable).
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q9B8D0-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q9B8D0-2; Sequence=VSP_006506;
CC -!- TISSUE SPECIFICITY: Highly expressed in spleen and testis;
CC detected at lower levels in lung and thymus.
CC -!- DISEASE: Defects in TNFRSF13C are a cause of severe B-cell
CC deficiency. B-cell deficient strain A/WySnJ has a 4.7 kb insertion
CC in the BAFFR gene leading to an altered C-terminus. The mutant RNA
CC is not detectable. B-cell lymphoproliferation is normal, but the life
CC span of peripheral B-cells is much reduced.
CC -!- SIMILARITY: Contains 1 TNFR-Cys repeat.
CC
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CC
CC EMBL; AF373847; AAK91827.1; -.
DR EMBL; AK008142; BAB25490.1; -.
DR MGD; MG:191299; Tfrsf13c.
KW Receptor; Immune response; Signal-anchor; Transmembrane; Glycoprotein;
KW Alternative splicing.
FT DOMAIN 1 71 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 72 92 SIGNAL-ANCHOR
FT DOMAIN 93 175 (TYPE III MEMBRANE PROTEIN) (POTENTIAL).
FT REPEAT 21 38 CYTOPLASMIC (POTENTIAL).
FT DISULFID 22 35 TNFR-CYS (PARTIAL).
FT BY SIMILARITY.

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FT DISULFID 27 38 BY SIMILARITY.
FT CARBOHYD 23 23 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 133 143 Missing (in isoform 2).
FT /FTid=VSP_006506.
SQ SEQUENCE 175 AA; 18798 MW; 288C7C1A02FB87EF CRC64;
Query Match 42.5%; Score 411; DB 1; Length 175;
Best Local Similarity 55.8%; Pred. No. 1.7e-21;
Matches 101; Conservative 9; Mismatches 55; Indels 16; Gaps 6;
QY 6 RSLGRDAPAPTPCVPAECFLLVHVCVACGLLTPRPKXGASSPAPRTALQPQESVG 65
DB 9 RSORGRDSVPTQNCQTECFDPLVRNCVSCLEFHP--DTGHTSLEPGTALQPQE-- 62
QY 66 AGAGAAALPLGCLLGCAGALLALVILV-LVGLVSWRRQRRLRGASAEAPDGDKDA 124
DB 63 ---GSAALPDVALLVGAALLLILALVLGLVLSVNRMQ-QLRAS----PDTSEGV 114
QY 125 -PEPLDKVILSPGISDATAPAWPPGDDGTTPPGHVSVPVPAELGSLTAVTTKTAGE 183
DB 115 QCESLENVFPSSSETPHASEPTWPLKEDADALSALPRHSVPVPAELGSLTAVTTKTAGE 174
QY 184 Q 184
DB 175 Q 175
RESULT 3
XP2_XENLA STANDARD; PRT; 439 AA.
AC P17437; Q08944;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Skin secretory protein xp2 precursor (APEG protein).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE OF 1-25 AND 344-439 FROM N.A. (ISOFORM 2).
RX MEDLINE=9232564; PubMed=1629230;
RA Hauser F., Roeben C., Hoffmann W.;
RT "xp2, a new member of the P-domain peptide family of potential growth
factors, is synthesized in Xenopus laevis skin."
RL J. Biol. Chem. 267:14451-14455(1992).
RN [2]
RP SEQUENCE OF 3-439 FROM N.A. (ISOFORM 1).
RC TISSUE=Skin;
RX MEDLINE=90127399; PubMed=2298293;
RA Gmachl M., Berger H., Thalhammer J., Kreil G.;
RT "Dermal glands of Xenopus laevis contain a polypeptide with a highly
repetitive amino acid sequence."
RL FEBS Lett. 260:145-148(1990).
CC -|- FUNCTION: MAY ACT AS A GROWTH FACTOR IN THE GERMAL LAYER OF THE
EPIDERMIS. MAY ALSO BE INVOLVED IN GROWTH OF REGENERATING GLANDS
AND IN PROTECTION OF THE SKIN FROM THE EXTERNAL ENVIRONMENT.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=APEG;
CC IsoId=p17437-1; Sequence=Displayed;
CC Name=2; Synonyms=XP2;
CC IsoId=p17437-2; Sequence=VSP_004652;
CC -|- TISSUE SPECIFICITY: SKIN.
CC -|- SIMILARITY: Contains 2 P-type (trefoil) domains.
CC -|- CAUTION: REF.2 SEQUENCE DIFFERS FROM THAT SHOWN FROM POSITION 392
ONWARD AND IS SHORTER (418 AA) DUE TO A FRAMESHIFT.
CC
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CC
DR EMBL; M90095; AAA50001.1; -
DR EMBL; X51394; CAA35759.1; ALT_FRAME.
DR PIR; A37331; A37331.
DR HSP; P04155; IFS2.
DR InterPro; IPR000519; P_trefoil.
DR Pfam; PF00088; trefoil_2.
DR PRINTS; PRO0680; PTREFOIL.
DR SMART; SM00018; PD; 2.
DR PROSITE; PS00025; P_TREFOIL; 2.
KW Signal; Growth factor; Alternative splicing; Repeat;
KW Pyridolone carboxylic acid. POTENTIAL.
FT SIGNAL 1 22
FT CHAIN 23 439 SKIN SECRETORY PROTEIN XP2.
FT MOD RES 23 23 PYRROLIDONE CARBOXYLIC ACID (PROBABLE).
FT DOMAIN 26 343 33 X REPEATS OF G-[GE]-[AE] (2,4)-A-E.
FT DOMAIN 350 391 P-TYPE 1.
FT DOMAIN 397 438 P-TYPE 2.
FT DISULFID 351 377 BY SIMILARITY.
FT DISULFID 361 376 BY SIMILARITY.
FT DISULFID 371 388 BY SIMILARITY.
FT DISULFID 398 424 BY SIMILARITY.
FT DISULFID 408 423 BY SIMILARITY.
FT DISULFID 418 435 BY SIMILARITY.
FT VARSPLIC 26 343 Missing (in isoform 2).
FT /FTid=VSP_004652.
FT CONFLICT 3 3 H -> S (IN REF. 2).
FT CONFLICT 18 18 C -> W (IN REF. 2).
SQ SEQUENCE 439 AA; 41173 MW; 38C4A4B57CBAE778 CRC64;
Query Match 12.3%; Score 118.5; DB 1; Length 439;
Best Local Similarity 26.0%; Pred. No. 0.2;
Matches 44; Conservative 10; Mismatches 58; Indels 57; Gaps 7;
QY 12 DAPATPC-----VPAECFDLLVHVCVACGLLTPRPKXG-ASSPAPRTALQPQES 63
DB 165 EAPAPAEAGEAPAPAEAG-----EAPAPAEAGEAPAPAEAGEAPAPA 210
QY 64 VGAGAGEAALPLGCLLGCAGALLALV-LVGLVSWRRQRRLRGASAEAP-DGDK 122
DB 211 PAPAEAGEAPAPAEAG-----EGEAPAPAEAGEA 238
QY 123 DAPEPLD-KVILSPGISDATAPAWPPGDDGTTPPGHVSVPVPAELG 170
DB 239 PAPAEAGEAPAPAEAGEAPAPA-PAEAGEAPAPAEAGEAPAPAEAG 286
RESULT 4
ICPO_HSVBJ STANDARD; PRT; 676 AA.
ID ICPO_HSVBJ
AC P29128;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Trans-acting transcriptional protein ICPO (P135 protein) (IER
DE 2.9/ER2.6).
GN BICFO.
OS Bovine herpesvirus type 1 (strain Jura).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirus.
OX NCBI_TaxID=31518;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=92219360; PubMed=3113901;
RA Wirth U.V., Fraefel C., Vogt B., Vlcek C., Schwyzler M.;
RT "Immediate-early RNA 2.9 and early RNA 2.6 of bovine herpesvirus 1
are 3' coterminal and encode a putative zinc finger transactivator
protein."
RT J. Virol. 66:2763-2772(1992).
RL

CC -1- P.TM: THE STRONGLY ACIDIC REGION MIGHT SERVE AS A TRANSCRIPTIONAL
CC ACTIVATION DOMAIN, POSSIBLY REGULATED THROUGH PHOSPHORYLATION BY
CC CASIN KINASE II.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -1- SIMILARITY: TO OTHER HERPESVIRUSES ICPO PROTEIN.
CC
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CC
CC EMBL: M84465; AAA46062.1; -
CC EMBL: AJ004801; CAA06138.1; -
CC PIR: B38209; EDBE23.
CC HSP: P28990; ICHC.
CC InterPro: IPR001841; Znf ring.
CC Pfam: PF000097; Zf-C3HC4; 1.
CC SMART: SM00184; RING; 1.
CC PROSITE: PS00518; ZF RING 1; 1.
CC PROSITE: PS00089; ZF RING 2; 1.
CC Transcription regulation; Trans-acting factor; Activator; Zinc-finger;
CC DNA-binding; Early protein; Repressor; Phosphorylation.
CC ZN FING 13 52 RING-TYPE.
CC DOMAIN 284 331 ASP/GLU-RICH (ACIDIC).
CC SEQUENCE 676 AA; 67879 MW; 11806B4E5C4EB71 CRC64;
CC
CC Query Match 12.0%; Score 116; DB 1; Length 676;
CC Best Local Similarity 30.8%; Pred. No. 0.43;
CC Matches 62; Conservative 13; Mismatches 82; Indels 44; Gaps 10;
CC
CC 7 SLRGDAPATPCVPACDFLLVHCVAC-----GLLRTPR-----PKPX 46
CC 353 STRGQTAVQAPRS-----LARRPCRAAASVPSRSRGRDRLPAPRAAPAAQ 408
CC
CC 47 AGASSPAPRTALQPSVSGAGAEALPLGLLFGAPALLGLALVVLVG----LVSWR 103
CC 409 ARACSPSPR-----EEGRGAGLVAAAGTAGWAGSEGRGERRARLLGEAGPPRVQARR 463
CC
CC 104 RQREL--RGASSAAPDGDKAPEPLDKVLIISPGISDATA-PAMPPGPDPTTPPGHS 161
CC 464 RRTELDRAPTAPAP---APAPAPISTVIDLT---ANAPAPADPAPAPAPGASAGA 517
CC
CC 162 VPVPATELSTELVTKTAP 182
CC 518 IGTEPA---AAAAVTAAP 534
CC
CC RESULT 5
CC HXB2 HUMAN STANDARD; PRT; 356 AA.
CC AC P14652; P10913; P17485;
CC DT 01-APR-1990 (Rel. 14, Created)
CC DT 01-APR-1990 (Rel. 14, Last sequence update)
CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
CC DE Homeobox protein Hox-B2 (Hox-2H) (Hox-2.8) (K8).
CC GN HXB2 OR HOX2H.
CC OS Homo sapiens (Human).
CC OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
CC NCBI_TaxID=9606;
CC RN [1]
CC
CC SEQUENCE FROM N.A.
CC RP MEDLINE=90098876; PubMed=2574852;
CC RA Acampora D., D'Esposito M., Faiella A., Pannese M., Migliacetto E.,
CC RA Morelli F., Stornaiuolo A., Nigro V., Simeone A., Boncinelli E.;
CC RT "The human HOX gene family."
CC RL Nucleic Acids Res. 17:10385-10402(1989).
CC RN [2]
CC
CC SEQUENCE OF 132-208 FROM N.A.
CC RP
CC TISSUE=Placenta;

RX MEDLINE=89378558; PubMed=2570724;
RA Giampaolo A., Acampora D., Zappavigna V., Pannese M.,
RA D'Esposito M., Care A., Faiella A., Stornaiuolo A., Russo G.,
RA Simeone A., Boncinelli E., Peschle C.;
RT "Differential expression of human HOX-2 genes along the anterior-
RT posterior axis in embryonic central nervous system."
RL Differentiation 40:191-197(1989).
RN [3]
RN
RN SEQUENCE OF 143-208 FROM N.A.
RP MEDLINE=90215256; PubMed=2576652;
RA Boncinelli E., Acampora D., Pannese M., D'Esposito M., Somma R.,
RA Gaudino G., Stornaiuolo A., Cafiero M., Faiella A., Simeone A.;
RT "Organization of human class I homeobox genes."
RL Genome 31:745-756(1989).
RN [4]
RN
RN SEQUENCE OF 143-202 FROM N.A.
RP MEDLINE=88329001; PubMed=2901346;
RA Kongsuwan K., Webb E., Housiaux P., Adams J.M.;
RT "Expression of multiple homeobox genes within diverse mammalian
RT haemopoietic lineages."
RL EMBO J. 7:2131-2138(1988).
RN [5]
RN
RN SEQUENCE OF 1-42 FROM N.A.
RP MEDLINE=95181447; PubMed=7876223;
RA Vieille-Grosjean I., Huber P.;
RT "Transcription factor GATA-1 regulates human HOX2 gene expression in
RT erythroid cells."
RL J. Biol. Chem. 270:4544-4550(1995).
CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- DEVELOPMENTAL STAGE: EXPRESSED IN WHOLE EMBRYOS AND FETUSES AT
CC 5-9 WEEKS FROM CONCEPTION.
CC -1- SIMILARITY: BELONGS TO THE ANTP HOMEBOX FAMILY.
CC PROSOPEDIA SUBFAMILY.
CC
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CC
CC EMBL: X16655; CAA34655.1; -
CC EMBL: X16176; CAA34298.1; -
CC EMBL: X14571; CAA32709.1; -
CC EMBL: X78978; CAA55581.1; -
CC PIR: S07542; WJHU2H.
CC HSP: P14653; I872.
CC TRANSFAC: T03323; -
CC Genew; HGNC:5113; HOXB2.
CC MIM; 142967; -
CC GO: GO:0008015; P.circulation; TAS.
CC GO: GO:0007275; P.development; TAS.
CC InterPro: IPR001827; Antennapedia.
CC InterPro: IPR001356; Homeobox.
CC InterPro: IPR000047; HTH lambrerepress.
CC Pfam: PF00046; homeobox_1
CC PRINTS; PR00025; ANTENNAPEDIA.
CC PRINTS; PR00024; HOMEBOX.
CC PRINTS; PR00031; HTHREPRESS.
CC ProDom; PD000010; Homeobox; 1.
CC SMART; SM00389; HOX; 1.
CC PROSITE; PS00027; HOMEBOX 1; 1.
CC PROSITE; PS00032; ANTENNAPEDIA; 1.
CC PROSITE; PS00071; HOMEBOX 2; 1.
CC Homeobox; DNA-binding; Developmental protein; Nuclear protein;
CC Transcription regulation.
CC SITE 94 99
CC DNA BIND 143 202
CC HOMEBOX.
CC ANTP-TYPE HEXAPEPTIDE.
CC PEA -> RRL (IN REF. 2).
CC CONFLICT 136 138
CC

SQ SEQUENCE 356 AA; 37913 MW; D7ACA0E3D5BBFB3 CRC64;
Query Match 11.9%; Score 115; DB 1; Length 356;
Best Local Similarity 24.7%; Pred. No. 0.28;
Matches 56; Conservative 15; Mismatches 68; Indels 88; Gaps 11;
QY 5 PRS-LRGRDAPA---PTPCVPAECFDLLVRHCVACGLLRTRP-----KPXA 47
DB 66 PRSQKAEADGAPALPPPPPPPLPA-----APPAFFPMKKEKSAKPSQ 109
QY 48 GASSAPRATLQPSVAGAGEALPLPG-----LL-----FG 81
DB 110 SATSPSAASAVFASGVGSPADGLPEAGGGGARRLRATYNTQLLEKEKPFHNKYL 169
QY 82 APALLGLALVLLVGLVSW--RRQRRLRGASAEAPDGDKAPFLDKVI-----I 133
DB 170 RPRVIAALLDTERQVQWQNRMKHKTQHQREPPDGEPCAGLEDICDPAEPA 229
QY 134 LSPGISDATAPAW-----PP-----EDPGTTTPG 159
DB 230 ASPGSPSAGRAAEACCHPEVVPVPGALSADPRPLAVRLEGAGASPG 276
RESULT 6
HCN4_MOUSE STANDARD; PRT; 1186 AA.
AC 070507;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Potassium/sodium hyperpolarization-activated cyclic nucleotide-gated
DE channel 4 (Brain cyclic nucleotide-gated channel 3) (BCNG-3).
GN HCN4 OR BCNG3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP CONCEPTUAL TRANSLATION OF 1-178 AND 685-1186.
RA Hinz U.;
RL Unpublished observations (FEB-2003).
RN [2]
RP SEQUENCE OF 179-684 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98292171; PubMed=9630217;
RA Santoro B., Liu D.T., Yao H., Bartsch D., Kandel E.R.,
RA Siegelbaum S.A., Tibbs G.R.;
RT "Identification of a gene encoding a hyperpolarization-activated
RT 'pacemaker' channel of brain."
RL Cell 93:717-729(1998).
RN [3]
RP FUNCTION, AND TISSUE SPECIFICITY.
RA MEDLINE=21530492; PubMed=11675786;
RA Stevens D.R., Seifert R., Bufe B., Mueller F., Kremer E., Gaus R.,
RA Meyerhof W., Kaupp U.B., Lindemann B.;
RT "Hyperpolarization-activated channels HCN1 and HCN4 mediate responses
RT to sour stimuli."
RL Nature 413:631-635(2001).
CC -!- FUNCTION: Hyperpolarization-activated ion channel with very slow
CC activation and inactivation exhibiting weak selectivity for
CC potassium over sodium ions. May contribute to the native pacemaker
CC currents in heart (If) and in neurons (Ih). Activated by cAMP (By
CC similarity). May mediate responses to sour stimuli.
CC -!- SUBUNIT: The potassium channel is probably composed of a homo- or
CC heterotetrameric complex of pore-forming subunits.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Detected in a subset of elongated cells in
CC taste buds.
CC -!- DOMAIN: The segment S4 is probably the voltage-sensor and is
CC characterized by a series of positively charged amino acids at
CC every third position.
CC -!- SIMILARITY: BELONGS TO THE POTASSIUM CHANNEL FAMILY. HCN
CC SUBFAMILY.

CC -!- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.
CC -!- CAUTION: The N- and the C-terminus are deduced from the genomic
CC sequence.
CC
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CC
CC EMBL; AF064874; AAC40126.1; -.
DR MGD; MGI:1298209; Hcn4.
DR InterPro; IPR000595; CNMP_binding.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR005820; M-channel_nlg.
DR Pfam; PF00027; CNMP_binding; 1.
DR Pfam; PF00520; ion_trans; 1.
DR SMART; SM00100; CNMP; 1.
DR PROSITE; PS00888; CNMP_BINDING_1; 1.
DR PROSITE; PS00889; CNMP_BINDING_2; FALSE_NEG.
DR PROSITE; PS00442; CNMP_BINDING_3; 1.
KW Transport; Ion transport; Ionic channel; Voltage-gated channel;
KW Potassium channel; Potassium; Potassium transport; Sodium transport;
KW cAMP; cAMP-binding; Transmembrane; Glycoprotein.
FT DOMAIN 1 266
FT TRANSMEM 267 287
FT TRANSMEM 294 314
FT DOMAIN 315 340
FT TRANSMEM 341 361
FT TRANSMEM 369 389
FT TRANSMEM 390 420
FT DOMAIN 421 441
FT TRANSMEM 442 466
FT TRANSMEM 467 517
FT TRANSMEM 518 1186
FT DOMAIN 519 520
FT DOMAIN 209 260
FT DOMAIN 784 1061
FT NP_BIND 595 712
FT CARBOHYD 458 458
FT SEQUENCE 1186 AA; 127413 MW; B3DC16818B8697DC CRC64;
Query Match 11.4%; Score 110.5; DB 1; Length 1186;
Best Local Similarity 27.4%; Pred. No. 1.7;
Matches 51; Conservative 17; Mismatches 73; Indels 45; Gaps 8;
QY 2 RRGP--RSLRGDAPAPTCVPAECFDLLVRHCVACGLLRTRPFPKXAGASSPAP----- 54
DB 40 RQDPGRRSIRLRPLSPSPSVAAGCSE---SRGAALGATESESGRSGAGKSTNGDCRRF 96
QY 55 RTALQPSVAGAGEALPLGLLFGAPALLGLALVLLVGLVSWRRQRRLRGASS 114
DB 97 RGLSLGSRGGGGGAG-----GSSSL-----GHLHDSAERLLAEG 136
QY 115 AEAPDGDKDAPEFLDKVILSPGISDATAPAWPPGPDGPTTPGHVVPVATLSTEL 174
DB 137 DASPGEDR-----TPDGL-ATEPERPATAPAAAPPPPPQPPQPPAS--ASCEQ 181
QY 175 VITKTA 180
DB 182 PSADTA 187
RESULT 7
T2D3_HUMAN STANDARD; PRT; 1083 AA.
ID T2D3_HUMAN
AC 000268; Q99721; Q9BR40; Q9BX42;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Transcription initiation factor TFIID 135 kDa subunit (TAFII-135)

Genew; HGNC:13918; BAT2.					
DR	MIM; 142580; -	GO; GO:0003822; F:MHC-interacting protein; TAS.			
DR	Repeat.				
KW	DOMAIN	519	524	POLY-PRO.	
FT	DOMAIN	636	657	GLN-RICH.	
FT	DOMAIN	684	688	POLY-PRO.	
FT	DOMAIN	699	704	POLY-PRO.	
FT	DOMAIN	814	821	POLY-PRO.	
FT	DOMAIN	1340	1345	POLY-GLY.	
FT	DOMAIN	1398	1403	POLY-GLY.	
FT	DOMAIN	1436	1442	POLY-PRO.	
FT	DOMAIN	1982	1991	POLY-PRO.	
FT	DOMAIN	41	1795	4 X 57 AA TYPE A REPEATS.	
FT	REPEAT	41	95	1-1.	
FT	REPEAT	98	154	1-2.	
FT	REPEAT	281	337	1-3.	
FT	REPEAT	1740	1795	1-4.	
FT	DOMAIN	337	549	2 X TYPE B REPEATS.	
FT	REPEAT	337	418	2-1.	
FT	REPEAT	476	549	2-2.	
FT	DOMAIN	1899	2089	3 X 50 AA TYPE C REPEATS.	
FT	REPEAT	1899	1948	3-1.	
FT	REPEAT	1965	2014	3-2.	
FT	REPEAT	2040	2089	3-3.	
PT	CONFLICT	57	57	R -> A (IN REF. 2).	
FT	CONFLICT	109	109	Q -> S (IN REF. 2).	
FT	CONFLICT	414	414	T -> K (IN REF. 2).	
FT	CONFLICT	532	532	Q -> K (IN REF. 2).	
FT	CONFLICT	682	682	E -> D (IN REF. 2).	
FT	CONFLICT	730	730	L -> R (IN REF. 2).	
FT	CONFLICT	750	750	A -> T (IN REF. 2).	
FT	CONFLICT	834	834	G -> A (IN REF. 2).	
FT	CONFLICT	1035	1035	M -> L (IN REF. 2).	
FT	CONFLICT	1068	1068	P -> R (IN REF. 2).	
FT	CONFLICT	1285	1285	G -> A (IN REF. 2).	
FT	CONFLICT	1400	1400	T -> S (IN REF. 2).	
FT	CONFLICT	1611	1611	G -> A (IN REF. 2).	
FT	CONFLICT	1729	1729	G -> A (IN REF. 2).	
SQ	SEQUENCE	2142 AA;	227840 MW;	32DDDF16B9B52420A CRC64;	
Query Match 10.9%; Score 105.5; DB 1; Length 2142;					
Best Local Similarity 24.9%; Pred. No. 6.1;					
Matches 46; Conservative 16; Mismatches 48; Indels 75; Gaps 10;					
QY	14	PAPTPCVPAFCFDLLVNRHVCACGLLTPRPKPKXAGASSPAPTALQPDSVGAGAGEAAL	73		
Dd	506	PAPPFAVPKE-----LPAPPAPPP--ASAPTEET--EPPEAQAPPAOST-	546		
QY	74	PLPLGFGAPALLGLALVLALVLGVLSWRRLRGASAADPDG-----D	121		
Dd	547	PTPGVA-AAPTLV-----GGSTSTSSSGSFASPVEPOLPS	583		
QY	122	XDAEPLDKVILLSPGISDATAPAWPPPEDCGTTPPGHSVVPVATLGSLVTTKTAG	181		
Dd	584	KEGPPEPEEV-----PPP ::: :::	623		
QY	182	-PEOQ	185		
Dd	624	YPKYQ	628		
RESULT 11					
DUS8 HUMAN					
ID	DUS8 HUMAN	STANDARD;	PRT;	625 AA.	
AC	Q13202;				
DT	15-JUL-1999	(Rel. 38, Created)			
DT	15-JUL-1999	(Rel. 38, Last sequence update)			
DT	28-FEB-2003	(Rel. 41, Last annotation update)			
DE	Dual specificity protein phosphatase 8 (EC 3.1.3.48) (EC 3.1.3.16)				
DE	Dual specificity protein phosphatase hVH-5).				
GN	DUSP8 OR VH5.				
OS	Homo sapiens (Human).				

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Petal brain;
 RX MEDLINE=96009533; PubMed=7561891;
 RA Martell K.J., Seasholtz A.F., Kwak S.P., Clemens K.K., Dixon J.E.;
 RT "NHV-5: a protein tyrosine phosphatase abundant in brain that
 RT inactivates mitogen-activated protein kinase.";
 RL J. Neurochem. 65:1823-1833(1995).
 CC -1- FUNCTION: THIS PROTEIN SHOWS BOTH ACTIVITY TOWARD TYROSINE-PROTEIN
 CC PHOSPHATE AS WELL AS WITH SERINE/THREONINE-PROTEIN PHOSPHATE (BY
 CC SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
 CC tyrosine + phosphate.
 CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
 CC phosphate.
 CC -1- TISSUE SPECIFICITY: ABUNDANT IN BRAIN, HEART, AND SKELETAL MUSCLE.
 CC -1- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
 CC TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.
 CC -1- SIMILARITY: Contains 1 rhodanese domain.
 CC
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 CC
 DR EMBL; U27193; AAA83151.1; -;
 DR HSSP; Q16828; IMKP.
 DR Genew; HGNC:3074; DUSP8.
 DR MIM; 602038; -;
 DR GO; GO:0005737; Cytoplasm; TAS.
 DR GO; GO:0004725; P:protein tyrosine phosphatase activity; TAS.
 DR GO; GO:0000188; P:inactivation of MAPK; TAS.
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.
 DR InterPro; IPR000340; DS_phosphatase.
 DR InterPro; IPR001763; Rhodanese-like.
 DR InterPro; IPR000387; Tyr_phosphatase.
 DR Pfam; PF00782; DSPC; 1.
 DR SMART; SM00195; DSPC; 1.
 DR SMART; SM00450; RHOD; 1.
 DR PROSITE; PS50206; RHODANES_3; 1.
 DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
 DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
 DR PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.
 KW Hydrolase; Nuclear protein.
 FT DOMAIN 23 138 RHODANES.
 FT DOMAIN 162 430 PROTEIN-TYROSINE PHOSPHATASE.
 FT DOMAIN 310 550 PRO-RICH.
 FT ACT SITE 246 246 BY SIMILARITY.
 SQ SEQUENCE 625 AA; 65840 MW; DCBEA14487219666 CRC64;
 Query Match 10.7%; Score 103.5; DB 1; Length 625;
 Best Local Similarity 32.9%; Pred. No. 2.8;
 Matches 53; Conservative 5; Mismatches 70; Indels 33; Gaps 8;
 QY 40 TPPEKPKXAGASSPAPRTALQVESVAGAGEAALPLGLFG----APALLGLALVLAIV 95
 Db TPEPPPPSPAGAPLPR--LPPTSESAAATGAAAREGLSAGGERPAPPTPTATSAALQQG 373
 QY 96 LVGL-VSWRRQ--RLRGA-----SSAEPDGDKDAPEPLD-----KVILL- 134
 Db LRGHLSSDLQDTNRLKRSFSDIKSAYAPSRPPDGPDPGEPAPKCLKLDSFGAAL 433
 QY 135 -----SFGISDATAPAMPPPGDPGTTTPPGHVSVPFATELG 170
 Db GLSFPSPDSDPAEAPRPRRRP-RFPAGSPARSPAHSLG 473

RESULT 12
 ICP4_HSVB STANDARD; PRT; 1487 AA.
 AC P28925;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE Trans-acting transcriptional protein ICP4 (155 kDa immediate-early
 DE protein).
 GN IE OR 64.
 OS Equine herpesvirus type 1 (strain Ab4p) (EHV-1).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Alphaherpesvirinae; Varicellovirus.
 OX NCBI_TaxID=31520;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92295566; PubMed=1318606;
 RA Telford E.A.R., Watson M.S., McBride K., Davison A.J.;
 RL "The DNA sequence of equine herpesvirus-1.";
 RL Virology 189:304-316(1992).
 CC -1- FUNCTION: THIS IE PROTEIN IS A MULTIFUNCTIONAL PROTEIN CAPABLE
 CC OF MIGRATING TO THE NUCLEUS, BINDING TO DNA, TRANS-ACTIVATING
 CC OTHER VIRAL GENES, AND AUTOREGULATING ITS OWN SYNTHESIS.
 CC -1- SUBCELLULAR LOCATION: NUCLEUS OF INFECTED CELLS.
 CC -1- FTM: A LONG STRETCH OF SERINE RESIDUES MAY BE A MAJOR SITE OF
 CC PHOSPHORYLATION.
 CC -1- SIMILARITY: BELONGS TO THE ICP4/IE140/IE180 FAMILY.
 CC
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 CC
 DR EMBL; M86664; AAB02515.1; -;
 DR EMBL; M86664; AAB02499.1; -;
 DR FIR; A38802; EDBEF6.
 DR TRANSFAC; T00401; -;
 DR InterPro; IPR005205; Herpes_ICP4_C.
 DR InterPro; IPR005206; Herpes_ICP4_N.
 DR Pfam; PF03585; Herpes_ICP4_C; 1.
 DR Pfam; PF03584; Herpes_ICP4_N; 1.
 KW Early protein; Transcription regulation; Trans-acting factor;
 KW DNA-binding; Phosphorylation; Nuclear protein.
 FT DOMAIN 181 213 SER-RICH.
 FT DOMAIN 922 931 ARG/LYS-RICH (BASIC).
 SQ SEQUENCE 1487 AA; 154868 MW; 1D4397838D03680D CRC64;
 Query Match 10.7%; Score 103.5; DB 1; Length 1487;
 Best Local Similarity 28.7%; Pred. No. 6;
 Matches 45; Conservative 11; Mismatches 62; Indels 39; Gaps 8;
 QY 12 DAPAPTPCV--PAECFDLLVHCVACGLLRTPRPKPXAGASSPAPRTALQVESVGAGAG 69
 Db DAPLSTPAVVIPPP-----SPTPEPRGGKAKRSPSAAGSGGPPPTAAAA 100
 QY 70 EALPLPGLLFGAPALLGLALVLAIVLGLVSWRRQRRLRGASSAEAPDGDKDAPEPLD 129
 Db QPASAP-----SPA-PGLAAMLVKWHSHSVAFNGR-----RATGSSSPGGDADPVALD 150
 QY 130 KVILLSPGISDA-TAPAPPPGDEFGTTTPPGHVSVPV 165
 Db -----SDTETCPGSPQ-EPFSSASPGGSPAP 177
 RESULT 13
 MED6_HUMAN STANDARD; PRT; 1003 AA.
 ID MED6_HUMAN
 AC Q96DN6; Q8N3M0; Q8NAB1; Q96Q00;
 DT 15-SEP-2003 (Rel. 42, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)

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DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Methyl-CpG binding domain protein 6.
GN MBD6 OR KIAA1887.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_
SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S.,
RA Fukuzumi Y., Fujimori Y., Komiyama M., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
RA Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A.,
RA Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K.,
RA Isegai T.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RN [2]_
SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA MEDLINE=21456161; PubMed=11572484;
RX Nagase T., Kikuno R., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XXI.
RT The complete sequences of 60 new cDNA clones from brain which code for
RT large proteins.";
RL large proteins.";
RN [3]_
SEQUENCE FROM N.A.
RC TISSUE=Amalgala;
RA Wambutt R., Heubner D., Mewes H.-W., Weil B., Wiemann S.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
CC -! SIMILARITY: Contains 1 methyl-binding (MBD) domain.
CC
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CC
CC EMBL; AK056399; BAB71176.1; -
CC EMBL; AK033078; BAC04045.1; -
CC EMBL; AB067474; BAB67780.1; -
CC EMBL; AL834230; CAD38908.1; -
CC Genew; HGNC:20445; MBD6.
CC InterPro; IPR001739; Methyl-CpG_bind.
CC SMART; SMO0391; MBD; 1.
CC DOMAIN 17 61 MBD.
CC FT DOMAIN 140 846 PRO-RICH.
CC FT CONFLICT 637 637 D -> G (IN REF. 1; BAB71176).
CC FT CONFLICT 802 802 Q -> Q (IN REF. 1; BAC04045).
CC SEQUENCE 1003 AA; 101200 MW; 6C8E8693AA6A3BB6 CRC64;
Query Match 10.7%; Score 103; DB 1; Length 1003;
Best Local Similarity 26.7%; Pred. No. 4.6; Mismatches 69; Indels 88; Gaps 13;
Matches 62; Conservative 13;
QY 4 GPRSLGRDAPATPCVPAECFDLLVRHCVACGLLTP-----RKPXAGASSP-A 53
DB 428 GSFNLLGSDAHLPPPTLSSGSPQPRHPQPSLPTTSGSLSSVPGAPAPPAASKADPV 487
QY 54 PRTALQ-POESVGNAGAE-----ALPLP-----GLLF-----CAPALLG-LALVIAL 94
DB 488 PSPVLQSPSEGLNGAGFACPLPLAGGEAFPPSPFQGLAUSGAGFGMLGALPLPLSL 547
QY 95 -----VLVGLVSWRRRORRLRGASSAEAPGDKDAPFPLDKVILSP--- 136
DB 548 GQPPPSPLNHSFGVLTG-----GSGQPPPEPL-----LPPFGG 582
QY 137 -----GISDATAFWPPGSD-----PGTTPGHVSP--VPATELGST 172
DB 583 PGPLAPCEPEGSLVSLVALLPPPSDLPPLPPSAPPNSNLLASFLPLLAGPT 634
RESULT 14
ICP4_HSVK
ID ICP4_HSVK STANDARD; PRT; 1487 AA.
AC P17473;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DE Trans-acting transcriptional protein ICP4 (155 kDa immediate-early
DE protein).
DE IE OR 64.
OS Equine herpesvirus type 1 (strain Kentucky A) (EHV-1).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirus.
OX NCBI_TaxID=10329;
RN [1]_
SEQUENCE FROM N.A.
RX MEDLINE=89370304; PubMed=2549711;
RA Grundy F.J., Baumann R.P., O'Callaghan D.J.;
RT "DNA sequence and comparative analyses of the equine herpesvirus type
RT 1 immediate early gene.";
RL Virology 172:223-236(1989).
RN [2]_
SEQUENCE OF 1432-1487 FROM N.A.
RX MEDLINE=90064773; PubMed=2555546;
RA Harty R.N., Colle C.F. III, Grundy F.J., O'Callaghan D.J.;
RT "Mapping the termini and intron of the spliced immediate-early
RT transcript of equine herpesvirus 1.";
RL J. Virol. 63:5101-5110(1989).
CC -! FUNCTION: THIS IS PROTEIN IS A MULTIFUNCTIONAL PROTEIN CAPABLE
CC OF MIGRATING TO THE NUCLEUS, BINDING TO DNA, TRANS-ACTIVATING
CC OTHER VIRAL GENES, AND AUTOREGULATING ITS OWN SYNTHESIS.
CC -! SUBCELLULAR LOCATION: NUCLEUS OF INFECTED CELLS.
CC -! PTM: A LONG STRETCH OF SERINE RESIDUES MAY BE A MAJOR SITE OF
CC PHOSPHORYLATION.
CC -! SIMILARITY: BELONGS TO THE ICP4/IE140/IE180 FAMILY.
CC
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CC
CC EMBL; J04366; AAA46089.1; -
CC EMBL; M30498; AAA66554.1; -
CC PIR; A33764; EDBE1.
CC InterPro; IPR005205; Herpes ICP4_C.
CC InterPro; IPR005206; Herpes ICP4_N.
CC Pfam; PF03585; Herpes ICP4_C; 1.
CC Pfam; PF03584; Herpes ICP4_N; 1.
CC Early protein; Transcription regulation; Trans-acting factor;
CC DNA-binding; Phosphorylation; Nuclear protein.
CC DOMAIN 181 213 SER-RICH.
CC FT DOMAIN 922 931 ARG/LYS-RICH (BASIC).
CC SEQUENCE 1487 AA; 154716 MW; 044E39A570608A6B CRC64;
Query Match 10.6%; Score 102.5; DB 1; Length 1487;
Best Local Similarity 28.7%; Pred. No. 7.1; Mismatches 62; Indels 39; Gaps 8;
Matches 45; Conservative 11;
QY 12 DAPAPTECV--PAECFDLLVRHCVACGLLTPRKPXAGASSPAPRTALQPOESVGNAGAG 69
DB 57 DAPLSTFVVVIPP-----SPAEPGKXKRSFSAAGSGPPTPAAA 100
QY 70 EALPLFGLLFGAPALLGLVLAFLVGLVSWRRRORRLRGASSAEAPGDKDAPFLD 129

```

Db 101 QPASPAP-----SPA-PGLAAMKLVHSSVAFNGR-----RATGSSSPGGGDAADPVALD 150
Qy 130 KVIILSPGISDA-TAPAWPPGDEGCTTPPGHSEVFP 165
Db 151 -----SDTETCPGSPQ-EPFSSASPGGSGSPAP 177

RESULT 15

ICPO_HSVBK STANDARD; PRT; 676 AA.
AC P29836;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-OCT-2001 (Rel. 40, Last annotation update)
DE Trans-acting transcriptional protein ICPO (P135 protein) (HER 2.9/ER2.6).
GN BICPO.
OS Bovine herpesvirus type 1 (strain K22).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirus.
OX NCBI_TaxID=31519;
RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE=92219360; PubMed=1313901;
RA Wirth U.V., Fraefel C., Vogt B., Vlcek C., Paces V., Schwyzler M.;
RT "Immediate-early RNA 2.9 and early RNA 2.6 of bovine herpesvirus 1
RT are 3' coterminal and encode a putative zinc finger transactivator
RT protein";
RL J. Virol. 66:2763-2772(1992).
CC -!- PFM: THE STRONGLY ACIDIC REGION MIGHT SERVE AS A TRANSCRIPTIONAL
CC ACTIVATION DOMAIN, POSSIBLY REGULATED THROUGH PHOSPHORYLATION BY
CC CASEIN KINASE II.
CC -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -!- SIMILARITY: TO OTHER HERPESVIRUSES ICPO PROTEIN.

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EMBL; M84464; AAA46061.1; -.
DR PIR; A38209; EDBE22.
DR HSSP; P28990; ICHC.
DR InterPro; IPR001841; Znf ring.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS00518; ZF_RING_1; 1.
DR PROSITE; PS00089; ZF_RING_2; 1.
KW Transcription regulation; Trans-acting factor; Activator; Zinc-finger;
KW DNA-binding; Early protein; Repressor; Phosphorylation.
FT ZN FING 13 52 RING-TYPE.
FT DOMAIN 284 331 ASP/GLU-RICH (ACIDIC).
SQ SEQUENCE 676 AA; 67701 MW; 9BB0683C9BFCA65D CRC64;

Query Match 10.8%; Score 102; DB 1; Length 676;
Best Local Similarity 29.9%; Pred. No. 3.8;
Matches 60; Conservative 14; Mismatches 83; Indels 44; Gaps 10;

Qy 7 SLRGSDAPPTPCVPAECFDLLVHCVAC-----GLLSTPR-----PKPX 46
Db 353 STRGRQTPAVQAPRS-----LAERPGRAAVSAAPSSRSRGREDPRLPAAPRAAPAQ 408
Qy 47 AGASSAPRPTALQFQSVGAGAEALPLGLLFGAPALLGLALVIALVLVG-----LVSWR 103
Db 409 ARACSPER-----EEGRGAGLVAAAGETAGVGVSEEGRGERRAKLLGEAGPPRVQARR 463
Qy 104 RRORRL--RGASSAEAPDGDADPEPLDKVILISPGISDATA-PAWPPPCEDPGTTPPGHS 161
Db 464 RRTELDRAPTAPAP---APAPAPISTWIDLT---ANAPAPADPAPAAALGAPALAGAQ 517

Qy 162 VPVPATELGGSTELVTTTKTGP 182
Db 518 IGTPA-----AAAAVTAATAAAP 534
Search completed: February 5, 2004, 17:59:34
Job time : 11.7778 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 5, 2004, 17:55:39, Search time 31.3472 Seconds
(without alignments)
1522.933 Million cell updates/sec

Title: US-10-045-574B-27

Perfect score: 966

Sequence: 1 MRGRPSLRGRDAPTPCV.....ATELGSTELVTYTKAGPEQ 185

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

SPTREMBL_23:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriap:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	411	42.5	175	11 Q8R4W8	Q8r4w8 mus musculu
2	118	12.2	348	4 Q8NFN3	Q8nfn3 homo sapien
3	117.5	12.2	552	10 Q96343	Q96343 brassica na
4	117.5	12.2	609	16 Q8FM53	Q8fm53 corynebacte
5	115.5	12.0	306	16 Q9EWE2	Q9ewe2 streptomyce
6	115	11.9	957	4 Q8TD92	Q8td92 homo sapien
7	115	11.9	991	4 Q9NCI5	Q9nci5 homo sapien
8	114.5	11.9	862	4 Q9NT23	Q9nt23 homo sapien
9	112.5	11.6	635	16 Q8N1V6	Q8n1v6 corynebacte
10	110.5	11.4	285	5 Q8SXU6	Q8sxu6 drosophila
11	110.5	11.4	285	5 Q8INT9	Q8int9 drosophila
12	110.5	11.4	625	5 Q9N5P3	Q9n5p3 caenorhabdi
13	110	11.4	530	11 Q8A276	Q8a276 mus musculu
14	108.5	11.2	221	16 Q8AD79	Q8ad79 streptomyce
15	108	11.2	575	16 Q8PJX1	Q8pjx1 xanthomonas
16	108	11.2	3247	12 Q85553	Q85553 bovine herp

17	107.5	11.1	895	10 Q9ARY0	Q9ary0 oryza sativ
18	107.5	11.1	1284	4 O15450	O15450 homo sapien
19	106.5	11.0	3084	12 Q8UZ11	Q8uz11 pseudorabie
20	105	10.9	675	11 Q91YM9	Q91ym9 mus musculu
21	105	10.9	1123	11 Q9DBD5	Q9dbd5 mus musculu
22	105	10.9	2116	12 Q99IE5	Q99ie5 rubella vir
23	105	10.9	2116	12 Q99IE7	Q99ie7 rubella vir
24	104.5	10.8	405	10 Q9AYM0	Q9aym0 oryza sativ
25	104.5	10.8	439	11 Q8BZY0	Q8bzy0 mus musculu
26	104	10.8	294	6 Q9MZV0	Q9mzv0 canis famli
27	104	10.8	480	10 Q8S2L2	Q8s2l2 oryza sativ
28	104	10.8	831	11 Q8VHF2	Q8vhf2 mus musculu
29	104	10.8	994	10 Q9ZR75	Q9zr75 selaginella
30	103.5	10.7	548	4 Q969H7	Q969h7 homo sapien
31	103.5	10.7	625	11 Q64213	Q64213 mus musculu
32	103.5	10.7	638	4 Q92744	Q92744 homo sapien
33	103.5	10.7	639	4 Q92745	Q92745 homo sapien
34	103.5	10.7	639	11 Q92124	Q92124 mus musculu
35	103.5	10.7	653	11 Q08817	Q08817 mus musculu
36	103.5	10.7	673	4 Q81Y00	Q81y00 homo sapien
37	103	10.7	437	6 Q29109	Q29109 sus scrofa
38	103	10.7	710	4 Q8N811	Q8n811 homo sapien
39	103	10.7	967	4 Q96Q00	Q96q00 homo sapien
40	103	10.7	1003	4 Q96DN6	Q96dne homo sapien
41	103	10.7	1212	16 Q9L1C8	Q9llc8 streptomyce
42	102.5	10.6	539	4 Q8N6Y3	Q8n6y3 homo sapien
43	102.5	10.6	548	4 Q14818	Q14818 homo sapien
44	102.5	10.6	623	4 Q14819	Q14819 homo sapien
45	102	10.6	356	11 Q88699	Q88699 mus musculu

ALIGNMENTS

RESULT 1

Q8R4W8 PRELIMINARY; PRT; 175 AA.
AC Q8R4W8; DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE TRAF3 binding protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Mizuno K., Irie S., Sato T.-A.;
RT "Identification of novel TRAF3 binding protein, T3BP, which increases
RT cellular F-actin content",
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF350257; AAL8394.1; -;
SQ SEQUENCE 175 AA; 18846 MW; B64EFF4B52EE93B1 CRC64;

Query Match 42.5%; Score 411; DB 11; Length 175;
Best Local Similarity 55.8%; Pred. No. 1.4e-25;
Matches 101; Conservative 9; Mismatches 55; Indels 16; Gaps 6;
QY 6 RSLGRDAPATPCVPACFPDLIVRHVCAGLLTTPPKPKXAGASSPAPTAIQPQESVG 65
DB 9 RSQRSDSVFTQCNOTCECFDLVRNCVSCLELFTPT---DTGHTSSLEPGTALQPOE--- 62
QY 66 AGAGAAALPLGLFGAPALLGLALVIALV-LVGLVSVRRQRRLRGASSAEPDGDKDA 124
DB 63 ---GSALRPDVALLVGAPALLGLILALTIVGLVSVRWQ-QLRITAS----PDISEGV 114
QY 125 -PEPLDKVILSPGISDATAPAPPPGDEGCTTPPHSHVVPATTELGSTELVTYTKAGPE 183
DB 115 QCESLENVFPVSSETPHASPATWPLKEDADSLPRHSPVPATTELGSTELVTYTKAGPE 174
QY 184 Q 184

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Db 175 Q 175
RESULT 2
Q96343 PRELIMINARY; PRT; 348 AA.
AC Q96343
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Neuregulin 1 isoform GGF2 (Fragment).
GN NRGL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RA Stefansson H., Sigurdsson E., Steinthorsdottir V., Bjornsdottir S.,
RA Sigurdsson T., Ghosh S., Brynjolfsson J., Gunnarsdottir S.,
RA Ivarsson O., Chou T.T., Hjalason O., Birgisdottir B., Jonsson H.,
RA Gudnadottir V.G., Gudmundsdottir E., Bjornsson A., Ingvarsson B.,
RA Ingason A., Sigfusson S., Hardardottir H., Harvey R.P., Brunner D.,
RA Mutel V., Gonzalo A., Lemke G., Sainz J., Johannesson G.,
RA Andersson T., Gudbjartsson D., Manculescu A., Frigge M.L., Gurney M.E.,
RA Kong A., Gulcher J.R., Petursson H., Stefansson K.,
RT "Neuregulin 1 and susceptibility to Schizophrenia".
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF491780; AAM71140.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_C2.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; IG_1.
DR SMART; SM00409; IG_1.
DR SMART; SM00408; IGC2; I.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin domain.
FT NON_TER 348 348
SQ SEQUENCE 348 AA; 36997 MW; 15568C6260C5635C CRC64;

Query Match 12.2%; Score 118; DB 4; Length 348;
Best Local Similarity 28.3%; Pred. No. 0.081;
Matches 54; Conservative 16; Mismatches 51; Indels 70; Gaps 11;

QY 2 RRGSRSLRGDAPPTPCVPAECFDLLVREHCACGLLTPRPKPXAGASSPAP-----54
Db 4 RRAFR-GRPGP-----RAQPGSAARSSPPLPLLL 38
QY 55 --RTALQPOESVGAGAGAAALPL-PCLLFCAPALLG-----LALVLALVLGVSVWRQR 107
Db 39 LGTALAP-----GAAGNEAPAGASVCYSPPSVGSVQELQRAAVVIEGKVHFORQQ 94
QY 108 ---RLGASSAEAP--DGDKDAPEPLDKVIIISPGISDATAP--AWPPFGEDF-----GT 155
Db 95 GALDKKAAAGAGAGANGDREPP-----AAGPRALGPPAESEPLLAANGT 139
QY 156 TPGHSHVVPVA 166
Db 140 VESNPTAEVPS 150

RESULT 3
Q96343 PRELIMINARY; PRT; 552 AA.
AC Q96343
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Myosinase-binding protein related protein (fragment).
OS Brassica napus (Rape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosid II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3708;
RN [1]
SEQUENCE FROM N.A.
RA STRAIN=20516 of Svalof's Karat;
RX MEDLINE=97210758; PubMed=9057822;
RA Taipaleensuu J., Falk A., Ek B., Rask L.;
RT "Myosinase-binding proteins are derived from a large wound-inducible
RT and repetitive transcript.";
RL Eur. J. Biochem. 243:605-611(1997).
DR EMBL; U59446; AAC08051.1; -.
DR HSSP; P18674; LJOT.
DR InterPro; IPR001229; Jacalin_lectin.
DR Pfam; PF01419; Jacalin; 3.
FT NON_TER 1 1
SQ SEQUENCE 552 AA; 59270 MW; 5F5E1A3718FBD0FA CRC64;

Query Match 12.2%; Score 117.5; DB 10; Length 552;
Best Local Similarity 28.8%; Pred. No. 0.14;
Matches 49; Conservative 5; Mismatches 59; Indels 57; Gaps 9;

QY 22 AECFDLLVREHCACGLLTPRPKPXAGASSPAPRTALQPOESVGAGAGAAALPLPGLLFG 81
Db 282 ADAIDALGAH---FGPLKTPAP-----SPAPGPAPAPAGSHAPAPAPAPAGP---329
QY 82 APALLGLALVLALVLVLVSVWRQRRLRGASSAEAPD-GDKDAPEPLDKVIIISPGISD 140
Db 330 -----QGRPAPAGAGPRPSPAP-----GPGPRP 354
QY 141 ATAPAWPPGPDGPTTP---PG---HSVP---VPATELGSTLVTKTAGP 182
Db 355 APAPA-PAPGQGRPAPGAPGQPHAPAAAGTATFAPAPTTKIGP 403

RESULT 4
Q96343 PRELIMINARY; PRT; 609 AA.
AC Q96343
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN CE2654.
OS Corynebacterium efficiens.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacteriaceae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=152794;
RN [1]
SEQUENCE FROM N.A.
RA STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
RA Kawarabayasi Y., Yamazaki J., Hino Y., Kikuchi H., Nakamura Y.,
RA Ikeo K., Suzuki M., Mashima J., Itoh T., Yamagishi A., Nishio Y.,
RA Ueda Y., Sugimoto S.;
RT "The entire genomic sequence of Corynebacterium efficiens YS-314."
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP005223; BAC19464.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 609 AA; 61385 MW; D127080D3874A578 CRC64;

Query Match 12.2%; Score 117.5; DB 16; Length 609;
Best Local Similarity 27.4%; Pred. No. 0.16;
Matches 52; Conservative 13; Mismatches 56; Indels 69; Gaps 10;

QY 10 GRDAPPTPCVPAECFDLLVREHCACGLLTPRPKPXAGASSPAPRTALQPOESVGAGAG 69
Db 35 GSAVAPAGGAVPP-----TVNG--PTQAPAPAGAAVAPATIPP-----AAPG 78
QY 70 EA-----ALPLPGLLFGA-----PALLGLALVLALVLVLVSVWRQRRLRGAS 113
Db 79 SAIPAPGAVTPTAVPTPGAAPAPAPATPTTPAAGSAIPAP-----GAA 121
QY 114 SAEA-PDGDKDAPEPLDKVIIISPGISDATAP-----AWPPPG-----EDPGT 155
Db 114 SAEA-PDGDKDAPEPLDKVIIISPGISDATAP-----AWPPPG-----EDPGT 155
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Db 122 TPTAVTPGSAITPTP--GAAVPAQVATPSARGASITPTPGAMPTPGTATPAGCAAPGA 179
Qy 156 TTPGHVVPV 165
Db 180 TTPGSAVPAP 189

RESULT 5
Q9WE2 PRELIMINARY; PRT; 306 AA.
AC Q9WE2;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein SC04865.
GN SC04865 OR SC20.06.
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomycetes.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphree L., Oliver K., O'Neill S.,
RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomycetes
RL Nature 417:141-147(2002).
DR EMBL; AL39121; CAC17653.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 306 AA; 23828 MW; FC67F6652FD0480B CRC64;

Query Match 12.0%; Score 115.5; DB 16; Length 306;
Best Local Similarity 27.1%; Pred. No. 0.11;
Matches 51; Conservative 13; Mismatches 75; Indels 49; Gaps 7;

Qy 8 LRGRDAPATPCVPACFDLLVHCVACGLLRTPKPKXAGASSPAPRTALQPOESVAG 67
Db 1 MRGAAGGPPADRAGAA-DWGARGHAGDGRDTPRPAQGVPTGTEALLAAALRAESAGTE 59
Qy 68 AGEAL- 103
Db 60 GERRALAAFAARDAPARAATRRRDDWRPRDGRHQRTPTALUSVLASLTGGVAY- 118
Qy 104 RRQRRLRGASSABAPDGDKAPEPLDKVILSPGISDATAPAMP---PPGEDPG----- 154
Db 119 ----AAAGGGGASDDGGDPTRP-----PAVSD-DAPARPAATPPGTPPGTGTGP 165
Qy 155 -TTPPGHS 161
Db 166 ATTPPGAS 173

RESULT 6
Q8TD92 PRELIMINARY; PRT; 957 AA.
AC Q8TD92;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hepatocellular carcinoma-associated protein HCA1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
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RN SEQUENCE FROM N.A.
RP Dong X., Chen W.;
RT "Identification of genes in the chromosome X that are differentially
RT expressed in hepatocellular carcinoma.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF490507; AAM08354.1; -.
DR InterPro; IPR002190; MAGE.
DR Pfam; PF01454; MAGE; 2.
DR PROSITE; PS50838; MAGE; 2.
SQ SEQUENCE 957 AA; 103253 MW; E09F9161384CC2B5 CRC64;

Query Match 11.9%; Score 115; DB 4; Length 957;
Best Local Similarity 26.1%; Pred. No. 0.4;
Matches 54; Conservative 23; Mismatches 90; Indels 40; Gaps 10;

Qy 5 PSLRGRDAPATPCVPACFDLLVHCVACGLLRTPKPKXAGASSPAPRT-----ALQ 59
Db 37 PADVPGSDVPGQ----PSDS-QILQGLCASEGPTSVLPSTSAEGPSTFVPPPTISEASSAS 91
Qy 60 PQESVAGAGAEALPLP--GLLFGAPALLGLALVLALVGLVSWRRRRQRLRGASSAEA 117
Db 92 GQPTISEGPTSVLPSTSEGLSTSGPTISKGLCTSVTLAA-----SEGRNTRSPPTSEE 147
Qy 118 PGDKDAPEPLDKV--ILSPGISDATAPAMP-----PGEDPGT-----TP- 157
Db 148 P--STSVPTASEVPTSLPPTPGEGTSTSVPTAYRGPSTSVVPTDGGFSTSVLPTPG 205
Qy 158 --PGHSVDPVPA TELGSTELVTTKAGP 182
Db 206 EGGTGVFLAATEGLSTSVQATPDGP 232

RESULT 7
Q9HC15 PRELIMINARY; PRT; 991 AA.
AC Q9HC15;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein KIAA1587.
GN KIAA1587.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20450683; PubMed=10997877;
RA Nagase T., Kikuno R., Nakayama M., Hiroseawa M., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes.
RT XVIII. The complete sequences of 100 new cDNA clones from brain which
RT code for large proteins in vitro.";
RL DNA Res. 7:273-281(2000).
DR EMBL; AB046807; BAB13413.1; -.
DR InterPro; IPR002190; MAGE.
DR Pfam; PF01454; MAGE; 2.
DR PROSITE; PS50838; MAGE; 2.
DR Hypothetical protein.
FT NON_TER
SQ SEQUENCE 991 AA; 106833 MW; 1DD36363402BAC81 CRC64;

Query Match 11.9%; Score 115; DB 4; Length 991;
Best Local Similarity 26.1%; Pred. No. 0.41;
Matches 54; Conservative 23; Mismatches 90; Indels 40; Gaps 10;

Qy 5 PSLRGRDAPATPCVPACFDLLVHCVACGLLRTPKPKXAGASSPAPRT-----ALQ 59
Db 71 PADVPGSDVPGQ----PSDS-QILQGLCASEGPTSVLPSTSAEGPSTFVPPPTISEASSAS 125
Qy 60 PQESVAGAGAEALPLP--GLLFGAPALLGLALVLALVGLVSWRRRRQRLRGASSAEA 117
Db 126 GQPTISEGPTSVLPSTSEGLSTSGPTISKGLCTSVTLAA-----SEGRNTRSPPTSEE 181
```

QY 118 PDGKDAPBPLDKV--IIISPGISDATAPAMP-----PCEDPGT-----TP- 157
Db 182 P--STSVPPTAGEVSTSLPPTGGTSTSVPTAYEGPSTSVVPTDEGGSVLTPTG 239
QY 158 --PGHSVPVPATLSTGLSTVLTTKTAGP 182
Db 240 EGGTSVPLAATLSTGLSTVQATPDEGP 266

RESULT 8

Q9NT23 Q9NT23 PRELIMINARY; PRT; 862 AA.
AC Q9NT23
DT 01-OCT-2000 (T-EMBLrel. 15, Created)
DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Hypothetical protein (Fragment).
GN DKFZP434A1010.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Dueterhoeft A., Lauber J., Mewes H.W., Gassenhuber J., Wiemann S.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL137579; CAB70821.1; -
DR HSP; Q07960; IRGP
DR InterPro: IPR000198; RhogAP.
DR Pfam: PF006620; RhogAP.1.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 862 AA; 90295 MW; 0DE275EB8CDB4A76 CRC64;

Query Match 11.9%; Score 114.5; DB 4; Length 862;
Best Local Similarity 27.0%; Pred. No. 0.39; 75; Indels 71; Gaps 11;
Matches 60; Conservative 16; Mismatches 16;
QY 10 GRDAP--APTTCVPAECFDLLVRHCVACGLLRTPRPKXA-----GASSPAPRTALQPOES 63
Db 328 GGPAPPASPAPAPASAF-----PPRVTPQAISPRGFTSPASPAALDISP 373
QY 64 -----VGAGAGEA-ALPLGLLFG--APALLGLALVLAIVGLVSWRRQR 107
Db 374 LAVSVPPAVLELLGAGAPASATPTPALSPGRSLRPLILLRGAEPILTDACQECMS 433
QY 108 RLRGASSAEAPDGDQDAPEPLDKVIIISPGISDATAPAMP----- 153
Db 434 KLRGAQGLGFDMSPLPPP--PLSLRFG--GAP--PPPPKPNPRLMALALAEAAQ 485
QY 154 -----GTTTPPGHSVPVP---ATELGSTELVTKTAGP 182
Db 486 VAEQSQOQECGGTTPPASQSPFHRSLSLVGGBLGTSGSGPP 527

RESULT 9

Q8NLV6 Q8NLV6 PRELIMINARY; PRT; 635 AA.
AC Q8NLV6
DT 01-OCT-2002 (T-EMBLrel. 22, Created)
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Hypothetical membrane protein Cgl2830.
GN Cgl2830.
OS Corynebacterium glutamicum (Brevibacterium flavum).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=1718;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;

RA Nakagawa S.;
RT "Complete genomic sequence of *Corynebacterium glutamicum* ATCC 13032.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP005283; BAC00224.1; -
DR InterPro: IPR002965; P-rich_extensin.
DR PRINTS; PR01217; PRICHEXTENS.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 635 AA; 66081 MW; ADFC4B8CE943C4EE CRC64;

Query Match 11.6%; Score 112.5; DB 16; Length 635;

Best Local Similarity 27.7%; Pred. No. 0.41; 62; Indels 47; Gaps 9;
Matches 49; Conservative 19; Mismatches 19;
QY 10 GRDAPAPTTCV--PAECFDLLVRHCVACGL-----LRTP---RKPXA-GASSPAPRTA 57
Db 74 GNAIPAPGGAIPPTPAKTEQDAVPTVAAKLPVPGSSIPAPGRALPTVPAPGGSVAPRAS 133
QY 58 LQPSVCGAGAGEAALPLPGL-LFCAPALLGLALVLAIVGLVSWRRQRRLGASSAE 116
Db 134 APAVENVPAAPG-AAVPAPGISIPAPASAPGSAI----- 166
QY 117 APDGDQDAPEPLDKVIIISPGIS--DATAPAMP-----DPGTPPGHSVPVPAT 167
Db 167 -PTPGTAIPVPGSATVPAPGVSPASGVPSIPVPGSVTPPAPGISAPGALPTPGS 222

RESULT 10

Q8SXU6 Q8SXU6 PRELIMINARY; PRT; 285 AA.
AC Q8SXU6
DT 01-JUN-2002 (T-EMBLrel. 21, Created)
DT 01-JUN-2002 (T-EMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE RE20756p.
GN BCDNA:RE20756.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkely;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe R., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George M., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S.,
Ratel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Ceiniker S.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY084128; AAL89866.1; -
DR FlyBase; FBgn0063685; BCDNA:RE20756.
DR InterPro: IPR006706; Extensin.2.
DR InterPro: IPR004019; YLP motif.
DR Pfam: PF04554; Extensin_2; 1.
DR Pfam: PF02757; YLP; 5.
SQ SEQUENCE 285 AA; 28614 MW; 66BA69FA334B4C3D CRC64;

Query Match 11.4%; Score 110.5; DB 5; Length 285;

Best Local Similarity 26.8%; Pred. No. 0.26;
Matches 44; Conservative 12; Mismatches 51; Indels 57; Gaps 7;
QY 11 RQAPAPTTC-----VPACFDLLVRHCVACGLLRTPRPKXPAGASSPAPETA-LQPOES 63
Db 138 QDIPAPAPAVTSAPAPAVTS-----APAPAVTSAPAPAVTSYELPVPQD 184
QY 64 VGAGAGEAALPLGLLFGAPALLGLALVLAIVGLVSWRRQRRLGASSAEAPDGDKD 123
Db 185 IPAPAVTSAPAPAVTSAPAPAV-----YSAPAP----- 215
QY 124 APEPLDKVIIISPGISDATAPAMP-----PGHSVPVPA 166
Db 216 APEYL-----PPVQDLFAPAPAVTSAPAPAVTSAPAPA 252

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

[3]

SEQUENCE FROM N.A.
RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
RA Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,
RA Tupy J.L., Bergman C., Carlson J.W., Celisner S.E.,
RA Klamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
RA Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,
RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
RT "Annotation of Drosophila melanogaster genome."
RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

[4]
SEQUENCE FROM N.A.
RN Adams M.D., Celisner S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
RP Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

[5]
SEQUENCE FROM N.A.
RN FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AB003669; AAN1105.1; - 66BAC35B38F5D2C CRC64;
SQ SEQUENCE 285 AA; 28554 MW; 66BAC35B38F5D2C CRC64;

Query Match 11.4%; Score 110.5; DB 5; Length 285;
Best Local Similarity 26.8%; Pred. No. 0.26;
Matches 44; Conservative 12; Mismatches 51; Indels 57; Gaps 7;

QY 11 RDAPATPC-----VPAECFDLLRHVCAGLLRTPKPKXGASSPAPRTA-LQPQS 63
DB 138 QDIAPAPAPVPYSAPAPVPYS-----APAPVPYSAPAPVPYSYLFPVQD 184
QY 64 VGAGAGAAALPLGLFCAPALLGLALVLALVLGLVSWRRORRLRGASSAAPDGKD 123
DB 195 IPAPVPYSAPAPVPYSAPAPVP-----YSAFAP-----YSAFAP----- 215

QY 124 APELDKVILSPGISDATPAMPPPGEDPGTTP-PCHSVPVDA 166
DB 216 APEYL-----PFVDLPAPAPVPYSAPAPVPYSAPAPA 252

RESULT 12
ID Q9NSP3 PRELIMINARY; PRT; 625 AA.
AC Q9NSP3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE Hypothetical protein H06I04.5.
GN H06I04.5.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditiida; Rhabditoidea;
OC Rhabditiidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RT Waterston R.;
RA "Genome sequence of the nematode C. elegans: a platform for
investigating biology." The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).

[2]
SEQUENCE FROM N.A.
RN STRAIN=Bristol N2;
RC STRAIN=Bristol N2;
RT "The sequence of C. elegans cosmid H06I04.";
RT Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC WATERSTON R.;
RA Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
RL EMBL; AC006651; AAF39870.3; -

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KW Hypothetical protein.
SQ SEQUENCE 625 AA; 69471 MW; CCB727C72CF84495 CRC64;

Query Match 11.4%; Score 110.5; DB 5; Length 625;
Best Local Similarity 24.6%; Pred. No. 0.59;
Matches 43; Conservative 24; Mismatches 79; Indels 29; Gaps 6;

QY 8 LRGRDAPPTPCVPASCDFLLVHVACGLLTTPRKPXAGASSPAPRTALQPSVAG 67
DB 64 LHRPPTTAPITPPK-----SOSPALPSPSPH-GASGAHAAPVTESPIKSTST 114
QY 68 AGAALPLPCLLFGAPALLGLALVIALVLGVSWRRRRLRGASSAEPDGDKDAPEP 127
DB 115 ASNAEASNVW---YIIGVVILLVIGIAFLIMRKKSK-PSSEVFPAPSAPEP 170
QY 128 LDKVILSPISDATAPAPPPGDDPTTPGHGVVPVATLGLSTELVTTKTAGP 182
DB 171 -----KPA-PKDPKDPKDPKDPKDPKDPKDPKDPKDPKDPKDPKDPKDP 209

RESULT 13
O88276 PRELIMINARY; PRT; 530 AA.
AC O88276
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE N-acetylglucosamine-6-O-sulfotransferase long form.
GN CHST2
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=98380482; PubMed=9712885;
RA Uchimura K., Muramatsu H., Kadonatsu K., Fan Q., Kurosawa N.,
RA Mitsuoka C., Kamagi R., Habuchi O., Muramatsu T.;
RA "Molecular cloning and characterization of an N-acetylglucosamine-6-O-
RT sulfotransferase.";
RT J. Biol. Chem. 273:22577-22583(1998).
DR EMBL; AB011452; BAA32138.1; -
DR EMBL; AB011452; BAA32139.1; -
DR EMBL; AB011451; BAA32137.1; -
DR MGD; MGI:1891160; Chst2.
DR InterPro; IPR00863; Sulfotransferase.
DR Pfam; PF00685; Sulfotransfer; 1.
KW Transferase.
SQ SEQUENCE 530 AA; 57814 MW; A113B1B735C363EC CRC64;

Query Match 11.4%; Score 110; DB 11; Length 530;
Best Local Similarity 29.1%; Pred. No. 0.55;
Matches 44; Conservative 16; Mismatches 61; Indels 30; Gaps 7;

QY 41 PRPKXAGASSPAPRTALQPSVAGAGEAALPLGLLFGAPALL---GLALVIALVLV 97
DB 15 PRPLPAAPA---AVQALLPPRRAGRWSPASPLGMKVFRRKALVLCAGYALLVLTML 71
QY 98 GLVSWRRRRLRGASSAEPDGDKDAPELDKVIILSPGISDATAPAPPPGDDPTTP 157
DB 72 NLLDYKWKKEFLQCCN---PDG-----PLGAAV-----GAAGAGNGRFGSPPAAPP 114
QY 158 PGHS-----VPV---PAVELGSTELVTTKTAG 181
DB 115 RAHSEMDPRTFYPPAGVAGVAAAGSAG 145

RESULT 14
Q9AD79
ID Q9AD79 PRELIMINARY; PRT; 221 AA.
AC Q9AD79
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
```

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DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE Putative membrane protein.
GN SCO4929 OR SK13.21C.
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
CX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RX MEDLINE=97000351; PubMed=8843436;
RA Redenbach M., Kieser H.M., Denapate D., Eichner A., Cullum J.,
RA Kinashi H., Hopwood D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL Mol. Microbiol. 21:77-96(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabinowitz E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RA "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
DR EMBL; AL939121; CAD30919.1; -
DR InterPro; IPR002965; P rich extensn.
DR PRINTS; PR01217; PRICEXTENS.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 221 AA; 21600 MW; 5E83A6C31AFCE89 CRC64;

Query Match 11.2%; Score 108.5; DB 16; Length 221;
Best Local Similarity 32.9%; Pred. No. 0.29;
Matches 47; Conservative 9; Mismatches 62; Indels 25; Gaps 8;

QY 39 RTRPKXAGASSPAPRTALQPSVAG-----AGEALPLPLGLFG---APALLGL 88
DB 71 RDPSPDP---ATAPAGTVGEFS---GAGSATSAMGLSGSPGLIPGLAPAPSATGP 124
QY 89 ALVLALV-LVGLVSWRRRRLRGASSAEPDGD---KDAPELDKVIILSPGISDATAP 144
DB 125 AVPLTAPVTRTPGAPETPKPGEGAGERERGGDTGTGERAPAGTP----QPSRDRFVP 180
QY 145 -AWPPRGEDPTTPGHVSVPVPA 166
DB 181 HVPVPPPPGFGTTPPSDPAPEPA 203

RESULT 15
Q8PUX1 PRELIMINARY; PRT; 575 AA.
ID Q8PUX1
AC Q8PUX1
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE N-acetylmuzaamoyl-L-alanine amidase.
GN AMIC OR XAC2406.
OS Xanthomonas axonopodis (pv. citri).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
CX NCBI_TaxID=92829;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=306 / ATCC 13902 / XV 101;
RX MEDLINE=22022145; PubMed=12024217;
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RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,
RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.P.,
RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities";
RL Nature 417:459-463(2002).
DR EMBL; AE011877; AM37258.1; --
DR InterPro; IPR002508; Amidase_3.
DR InterPro; IPR000104; Antifreeze_1.
DR InterPro; IPR002985; P-rich_extensn.
DR Pfam; PF01520; Amidase_3; 1.
DR PRINTS; PR00308; ANTIFREEZE1.
DR PRINTS; PR01217; PRICHEXTENS.
KW Complete proteome.
SQ SEQUENCE 575 AA; 57723 MW; 614EC7392308CC93 CRC64;

Query Match 11.2%; Score 108; DB 16; Length 575;
Best Local Similarity 26.0%; Pred.No. 0.86;
Matches 50; Conservative 13; Mismatches 83; Indels 46; Gaps 7;

QY 14 PAPTQCVPAECFDLL-----VRHCVACGLLRTPRPKPKXAGASSPAPRTALQPOESVGAGAG 69
DB 192 PPAPSVPASAMETVTOAPVPTTIATG-VPTFRPATSTTGCAPAPTGVAGTPTNRAGAA 250
QY 70 EAALPLGLLFGAPALLGLALVLVLVGLVSWRRRRRLRGASSAEPDGDADP----- 125
DB 251 -AAPPSGAVVAGSAAAAAILNGSGAPMGATSGNAGAIAPNSAGSWGVAAGDDDLPPRPV 309
QY 126 -----BFLDKVILSPGISDATAPAWPPPPGDPGTTTPGHSPVPATELGS 171
DB 310 LPSEASRIKQAFGMRL--VVAIDFGH-----GQDPGANGP-----TGK 347
QY 172 TELVTTKTAGE 183
DB 348 REKDVTLAVGRE 359

Search completed: February 5, 2004, 18:00:48
Job time : 33.3472 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 5, 2004, 17:49:14 ; Search time 38.5417 Seconds
(without alignments)
761.888 Million cell updates/sec

Title: US-10-045-574B-27

Perfect score: 966

Sequence: 1 MRRGRSLRGRDAPAPPCV.....ATELGSTELVTTKTAGPEQQ 185

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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24: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	955	98.9	185	AAE22242	Human mature JST57
2	954.5	98.8	184	ABB81483	Human Ztnfr12 prot
3	954.5	98.8	184	AAE35227	Human Ztnfr12 rece
4	954.5	98.8	184	ABP97721	Amino acid sequenc
5	954.5	98.8	266	AAE22243	Human JST576 (BAFF
6	948	98.1	185	AAE22270	Human BAFF recepto
7	947	98.0	185	AAE22271	Human BAFF recepto
8	944	97.7	185	AAE22268	Human BAFF recepto
9	940	97.3	185	AAE22269	Human BAFF recepto

10	936	96.9	185	23	AAE22267	Human BAFF recepto
11	929	96.2	185	23	AAE22266	Human BAFF recepto
12	411	42.5	175	23	ABB78398	Amino acid sequenc
13	411	42.5	175	23	ABB81489	Mouse Ztnfr12 prot
14	411	42.5	175	23	AAE22244	Murine BAFF recept
15	411	42.5	175	24	ABP97722	Amino acid sequenc
16	377.5	39.1	320	23	AAE22245	Murine IgG-kappa s
17	373.5	38.7	328	23	ABB81493	Ztnfr12-tcs-FCS fu
18	364.5	37.7	70	23	AAE22246	Human BAFF-R:Fc fu
19	357.5	37.0	70	23	AAE22258	Human BAFF-R:Fc cl
20	357.5	37.0	70	23	AAE22265	Human BAFF-R:Fc cl
21	356.5	36.9	70	23	AAE22264	Human BAFF-R:Fc cl
22	353.5	36.6	70	23	AAE22262	Human BAFF-R:Fc cl
23	352.5	36.5	70	23	AAE22260	Human BAFF-R:Fc cl
24	351.5	36.4	70	23	AAE22259	Human BAFF-R:Fc cl
25	350.5	36.3	70	23	AAE22255	Human BAFF-R:Fc cl
26	349.5	36.2	70	23	AAE22257	Human BAFF-R:Fc cl
27	349.5	36.2	70	23	AAE22263	Human BAFF-R:Fc cl
28	346.5	35.9	70	23	AAE22253	Human BAFF-R:Fc cl
29	345.5	35.8	70	23	AAE22256	Human BAFF-R:Fc cl
30	345.5	35.8	70	23	AAE22261	Human BAFF-R:Fc cl
31	342.5	35.5	70	23	AAE22254	Human BAFF-R:Fc cl
32	338.5	35.0	70	23	AAE22252	Human BAFF-R:Fc cl
33	326.5	33.8	73	23	AAE22248	Human BAFF-R:Fc cl
34	306.5	31.7	73	23	AAE22249	Human BAFF-R:Fc cl
35	280.5	29.0	73	23	AAE22250	Human BAFF-R:Fc cl
36	273.5	28.3	73	23	AAE22251	Human BAFF-R:Fc cl
37	178	18.4	38	24	ABJ38415	TALL-1 related pep
38	142.5	14.8	65	23	AAE22247	Mouse BAFF-R:Fc fu
39	123	12.7	422	17	AAE87467	Glial growth facto
40	120	12.4	19938	24	ABP76681	Streptomyces virid
41	118	12.2	248	15	AAE46912	GGF segment E. Ho
42	118	12.2	248	15	AAE55653	GGF segment E. Ho
43	118	12.2	248	17	AAW09358	Human glial growth
44	118	12.2	248	17	AAE96074	Human glial growth
45	118	12.2	248	17	AAE87445	Human glial growth

ALIGNMENTS

RESULT 1
AAE22242
ID AAE22242 standard; Protein; 185 AA.
XX AAE22242;
XX AC AC
XX 25-JUL-2002 (first entry)
XX DE Human mature JST576 (BAFF-R) protein.
XX KW Human; BAFF receptor; BAFF-R; cytostatic; hypotensive; inflammation; TNF;
KW Tumour Necrosis Factor; autoimmune disease; immunosuppressive; cancer;
KW myasthenia gravis; hypertension; organ transplantation; drug screening;
KW HIV; human immunodeficiency virus; Genetic disorder; cardiovascular;
KW renal; rheumatoid arthritis; systemic lupus erythematosus; amyloidosis;
KW haemolytic anaemia; Chagas' disease; Grave's disease; glomerulonephritis;
KW Multiple myeloma; chromosomal mapping; tissue typing; drug screening;
JST576.
XX KW
XX OS Homo sapiens.
XX FH Key
XX Key Domain Location/Qualifiers
FT 19..35 /note= "Four cysteine motif"
FT Misc-difference 49 /note= "Alternative splice acceptor site"
FT Region 72..100 /note= "Hydrophobic region"
FT Domain 73..100 /label= Transmembrane_domain
FT Region 105..108 /note= "Stop transfer signal"

XX WO200224903-A2.
XX 28-MAR-2002.
XX
XX 06-SEP-2001; 2001WO-US28006.
XX
XX 18-SEP-2000; 2000US-233152P.
XX 21-SEP-2000; 2000US-234140P.
XX 13-FEB-2001; 2001US-268499P.
XX 14-AUG-2001; 2001US-312185P.
XX (BIOJ) BIOGEN INC.
XX
XX Ambrose CM, Thompson JS;
XX
XX WPI; 2002-362428/39.
XX N-PSDB; AAD35409.
XX
XX New human BAF-R receptor proteins and nucleic acids, useful for
PT treating, preventing or delaying e.g. autoimmune diseases, cancers,
PT inherited genetic disorders involving B-cells, cardiovascular
PT disorders, or renal disorders -
XX
XX Claim 1; Fig 2d; 164pp; English.
XX
XX The invention relates to human BAF-R receptor (BAF-R) nucleic acids and
CC proteins. BAF-R is a B-cell activating factor belonging to the tumour
CC Necrosis Factor (TNF) family, which is associated with the expression of
CC B-cells and immunoglobulins. The BAF-R proteins, DNA and antibodies are
CC useful for treating, preventing or delaying autoimmune diseases, cancer,
CC tumorigenic conditions or inherited genetic disorders involving B-cells,
CC hypertension, cardiovascular disorders, immunosuppressive diseases, renal
CC disorders, inflammation, organ transplantation and HIV. Autoimmune
CC diseases, which can be treated or prevented by BAF-R, include systemic
CC lupus erythematosus, rheumatoid arthritis, myasthenia gravis, autoimmune
CC haemolytic anaemia, idiopathic thrombocytopenia purpura, Chagas' disease
CC Grave's disease, anti-phospholipid syndrome, Wegener's granulomatosis,
CC poly-arthritis nodosa and rapidly progressive glomerulonephritis. Plasma
CC cells disorders e.g., multiple myeloma, Waldenstrom's macroglobulinaemia,
CC heavy-chain disease, primary or immunocyte-associated amyloidosis, and
CC monoclonal gammopathy of undetermined significance. The nucleic acids,
CC protein, protein homologues, and antibodies may further be used in
CC screening assays, in detection assays (chromosomal mapping, tissue typing
CC or forensic biology), predictive medicine (e.g. diagnostic or prognostic
CC assays, monitoring clinical trials, or pharmacogenomic). The polypeptides
CC are further useful as immunogens to raise anti-BAF-R antibodies, or in
CC screening drugs or compounds that modulate BAF-R activity or expression.
CC The present sequence is human mature J5T576 (BAF-R) protein.
XX
XX Sequence 185 AA;
SQ

Query Match 98.9%; Score 955; DB 23; Length 185;
Best Local Similarity 98.4%; Pred. No. 7e-73;
Matches 182; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MRGRPSLRGDAAPTPCPVPAECFDLLVHVCVACGLLRTPKPKVAGASSAPATLQP 60
Db 1 MRGRPSLRGDAAPTPCPVPAECFDLLVHVCVACGLLRTPKPKVAGASSAPATLQP 60
QY 61 QESVVGAGAGEAALPLGILLFGAPALLGLALVLAIVLVGLVSWRRQRRLRGASSAEAPDG 120
Db 61 QESVVGAGAGEAALPLGILLFGAPALLGLALVLAIVLVGLVSWRRQRRLRGASSAEAPDG 120
QY 121 KDAAPEPLDKVILSPGISDATAPAWPPGDDGTPPGHVSVPVPA TELGSTELVTTKTA 180
Db 121 KDAAPEPLDKVILSPGISDATAPAWPPGDDGTPPGHVSVPVPA TELGSTELVTTKTA 180
QY 181 GPEQQ 185
Db 181 GPEQQ 185

RESULT 2
ABB81483
ID ABB81483 standard; Protein; 184 AA.
XX
XX ABB81483;
AC
DT 02-SEP-2002 (first entry)
XX
DE Human Ztnfr12 protein SEQ ID NO:2.
XX
XX Human; Ztnfr12; tumour necrosis factor receptor; cytostatic;
KW immunosuppressive; dermatological; antiinflammatory; antidiabetic;
KW neuroprotective; antirheumatic; antiarthritic; antiasthmatic;
KW nephrotropic; hypotensive; gene therapy; B lymphocyte; tumour;
KW autoimmune disorder; systemic lupus erythematosus; myasthenia gravis;
KW multiple sclerosis; insulin dependent diabetes mellitus; asthma;
KW rheumatoid arthritis; bronchitis; emphysema; renal disease; lymphoma;
KW glomerulonephritis; vasculitis; chronic lymphoid leukaemia; nephritis;
KW pyelonephritis; renal neoplasm; multiple myeloma; amyloidosis;
KW light chain neuropathy; hypertension; large vessel disease;
KW graft-versus host disease; graft rejection; Crohn's disease;
KW chromosome 22q13.2.
XX
XX Homo sapiens.
OS
XX WO200238766-A2.
PN
XX 16-MAY-2002.
PD
XX 05-NOV-2001; 2001WO-US47018.
XX
XX 07-NOV-2000; 2000US-246449P.
XX 20-DEC-2000; 2000US-257131P.
XX 28-JUN-2001; 2001US-301715P.
XX 29-AUG-2001; 2001US-315565P.
XX (ZYMO) ZYMOGENETICS INC.
XX
XX Gross JA, Xu W, Henne RM, Grant FJ;
PI WPI; 2002-508212/54.
DR N-PSDB; ABB94426.
DR
XX Novel isolated human tumour necrosis factor receptor polypeptide, termed
PT Ztnfr 12, useful for treating autoimmune disorders, emphysema, end
PT stage renal failure or renal disease and lymphoma -
XX
XX Claim 3; Page 133; 154pp; English.
XX
XX The present sequence represents a human tumour necrosis factor receptor
CC designated Ztnfr12 (1). (1) has cytostatic, immunosuppressive,
CC dermatological, antiinflammatory, neuroprotective, antidiabetic,
CC antirheumatic, antiarthritic, antiasthmatic, nephrotropic and hypotensive
CC activities, and can be used in gene therapy. (1) can be used for
CC inhibiting, in a mammal, the activity of a ligand that binds Ztnfr12
CC (e.g. ZTNF4), for treating disorders and diseases associated with B
CC lymphocytes, activated B lymphocytes or resting B lymphocytes, and for
CC inhibiting the proliferation of tumour cells. (1) is useful for treating
CC autoimmune disorders such as systemic lupus erythematosus, myasthenia
CC gravis, multiple sclerosis, insulin dependent diabetes mellitus, asthma,
CC rheumatoid arthritis, bronchitis, emphysema and end stage renal failure
CC or renal disease such as glomerulonephritis, vasculitis, chronic lymphoid
CC leukaemia, nephritis, and pyelonephritis, and for treating renal
CC neoplasms, multiple myelomas, lymphomas, light chain neuropathy, or
CC amyloidosis, hypertension, large vessel diseases, graft-versus host
CC disease, graft rejection and Crohn's disease. (1) is useful for
CC modulating the immune system, for regulating B cell responses and
CC development, for modulating development of other cells, antibody
CC production and cytokine production, and for modulating T and B cell
CC communication. Human Ztnfr12 is located to chromosome 22q13.2.
XX
XX Sequence 184 AA;
SQ

Query Match 98.8%; Score 954.5; DB 23; Length 184;
Best Local Similarity 99.5%; Pred. No. 7.7e-73;
Matches 184; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MRGPRSLRGRDAPATPCVPAECFDLLVRHCVACGLLRTPRPKXPAGASSPAPRTALQP 60
DB 1 MRGPRSLRGRDAPATPCVPAECFDLLVRHCVACGLLRTPRPKXPAGASSPAPRTALQP 59
QY 61 QESVGAGAGEAALPLPGLLFGAPALLGLALVLVLVGLVSWRRQRRLRGASSAEAPDG 120
DB 60 QESVGAGAGEAALPLPGLLFGAPALLGLALVLVLVGLVSWRRQRRLRGASSAEAPDG 119
QY 121 DKDAPEPLDKVILSPGISDATAPAWPPGDPGTPPGHSPVPATLSTELVTTKTA 180
DB 120 DKDAPEPLDKVILSPGISDATAPAWPPGDPGTPPGHSPVPATLSTELVTTKTA 179
QY 181 GPEQQ 185
DB 180 GPEQQ 184

RESULT 3
AAE35227
ID AAE35227 standard; Protein; 184 AA.
XX AC AAE35227;
XX DE 28-MAY-2003 (first entry)
XX DT Human Ztnfr12 receptor protein.
XX DE Transmembrane activator; calcium modulator; nephrotropic; antibacterial;
XX KW TAC1; tumour necrosis factor-like protein; ZTNF2; ZTNF4; immunoglobulin;
XX KW anaemia; gene therapy; cytostatic; antiinflammatory; immunosuppressive;
XX KW glomerulonephritis; asthma; bronchitis; graft rejection; septic shock;
XX KW dermatological; neuroprotective; cyclophilin ligand-interactor; human;
XX KW autoimmune disease; systemic lupus erythematosus; multiple sclerosis;
XX KW diabetes mellitus; rheumatoid arthritis; renal disease; inflammation;
XX KW Ztnfr12; receptor.
XX OS Homo sapiens.
XX PN WO200294852-A2.
XX PD 28-NOV-2002.
XX PF 20-MAY-2002; 2002WO-US15910.
XX PR 24-MAY-2001; 2001US-293343P.
XX PA (ZYMO) ZYMOGENETICS INC.
XX PI Rixon MW, Gross JA;
XX DR WPI; 2003-148455/14.
XX DR N-PSDB; AAE33776.
XX PT Transmembrane activator and calcium modulator and cyclophilin
XX PT ligand-interactor (TAC1)-immunoglobulin fusion protein, for treating
XX PT cancer or diabetes, comprises a TAC1 receptor group and an
XX PT immunoglobulin group -
XX PS Disclosure; Column 136-137; 71pp; English.
XX CC The invention relates to fusion proteins comprising transmembrane
XX CC activator and calcium modulator and cyclophilin ligand-interactor (TAC1)
XX CC receptor group that binds tumour necrosis factor-like protein (ZTNF)2 or
XX CC ZTNF4; and an immunoglobulin group comprising a constant region of an
XX CC immunoglobulin. The invention is used to manufacture a medicament for
XX CC inhibiting the proliferation of tumour cells in a mammalian subject.
XX CC The composition comprising the fusion protein may also be used in
XX CC treating autoimmune diseases (e.g. systemic lupus erythematosus,
XX CC multiple sclerosis, diabetes mellitus, rheumatoid arthritis and asthma),

CC renal diseases (e.g. glomerulonephritis), bronchitis, inflammation,
CC graft rejection, anaemia and septic shock. The fusion proteins are
CC also used in gene therapy. The present sequence is human Ztnfr12
CC receptor protein.
XX Sequence 184 AA;
SQ

Query Match 98.8%; Score 954.5; DB 24; Length 184;
Best Local Similarity 99.5%; Pred. No. 7.7e-73;
Matches 184; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MRGPRSLRGRDAPATPCVPAECFDLLVRHCVACGLLRTPRPKXPAGASSPAPRTALQP 60
DB 1 MRGPRSLRGRDAPATPCVPAECFDLLVRHCVACGLLRTPRPKXPAGASSPAPRTALQP 59
QY 61 QESVGAGAGEAALPLPGLLFGAPALLGLALVLVLVGLVSWRRQRRLRGASSAEAPDG 120
DB 60 QESVGAGAGEAALPLPGLLFGAPALLGLALVLVLVGLVSWRRQRRLRGASSAEAPDG 119
QY 121 DKDAPEPLDKVILSPGISDATAPAWPPGDPGTPPGHSPVPATLSTELVTTKTA 180
DB 120 DKDAPEPLDKVILSPGISDATAPAWPPGDPGTPPGHSPVPATLSTELVTTKTA 179
QY 181 GPEQQ 185
DB 180 GPEQQ 184

RESULT 4
ABP97721
ID ABP97721 standard; Protein; 184 AA.
XX AC ABP97721;
XX DT 28-MAY-2003 (first entry)
XX DE Amino acid sequence of human BR3 receptor.
XX KW Human; TAC1; BR3; receptor; tumour necrosis factor ligand; TNF ligand;
XX KW TALL-1; April; systemic lupus erythematosus.
XX OS Homo sapiens.
XX PN WO2003014294-A2.
XX PD 20-FEB-2003.
XX PF 24-JUL-2002; 2002WO-US23487.
XX PR 03-AUG-2001; 2001US-310114P.
XX PR 30-APR-2002; 2002US-377171P.
XX PA (GETH) GENENTECH INC.
XX PI Dixit V, Grewal I, Ridgway J, Yan M;
XX DR WPI; 2003-248010/25.
XX PT New nucleic acid encoding a TAC1s or BR3 polypeptide, useful for
XX PT preparing a composition for treating systemic lupus erythematosus -
XX PS Claim 35; Fig 6B; 153pp; English.
XX CC The present sequence represents a human BR3 polypeptide. The
XX CC specification also describes TAC1 polypeptides. TAC1 and BR3 are
XX CC receptors. Tumour necrosis factor (TNF) family ligands TALL-1 and
XX CC April bind to the TAC1 receptor, while TNF family ligands TALL-1 also
XX CC binds to BR3 receptor. The TAC1 and BR3 receptor nucleic acid is useful
XX CC for preparing a composition for treating systemic lupus erythematosus.
XX Sequence 184 AA;
SQ

Query Match 98.8%; Score 954.5; DB 24; Length 184;

Best Local Similarity 99.5%; Pred. No. 7.7e-73;
Matches 184; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 MRGPRSLRGDRDAPATPCVPAECFOLLVHVCVACGLLTPRPKPXAGASSPAPRTALQP 60
Db 1 MRGPRSLRGDRDAPATPCVPAECFOLLVHVCVACGLLTPRPKPXAGASSPAPRTALQP 59
QY 61 QESVAGAGAGEAALPLPGLLFGAPALLGLALVLVGLVSWRRQRRLRGASSAEAPDG 120
Db 60 QESVAGAGAGEAALPLPGLLFGAPALLGLALVLVGLVSWRRQRRLRGASSAEAPDG 119
QY 121 DKDAPELDKVIILSPGISDATAPAMPPEGPCTTPPGHVSVPVPAELGSELVTTKTA 180
Db 120 DKDAPELDKVIILSPGISDATAPAMPPEGPCTTPPGHVSVPVPAELGSELVTTKTA 179
QY 181 GPEEQ 185
Db 180 GPEEQ 184

RESULT 5
AAE22243
ID AAE22243 standard; Protein; 266 AA.
XX
AC AAE22243;
DT 25-JUL-2002 (first entry)
XX
DE Human JST576 (BAFF-R) cDNA spliced version encoded protein.
XX
KW Human; BAFF receptor; BAFF-R; cytostatic; hypotensive; inflammation; TNF;
KW Tumour Necrosis Factor; autoimmune disease; immunosuppressive; cancer;
KW Myasthenia gravis; hypertension; organ transplantation; drug screening;
KW HIV; human immunodeficiency virus; genetic disorder; cardiovascular;
KW renal; rheumatoid arthritis; systemic lupus erythematosus; amyloidosis;
KW haemolytic anaemia; Chagas' disease; Grave's disease; glomerulonephritis;
KW multiple myeloma; chromosomal mapping; tissue typing; drug screening;
JST576.
XX
OS Homo sapiens.
XX
PN WO200224909-A2.
XX
PD 28-MAR-2002.
XX
PF 06-SEP-2001; 2001WO-US28006.
XX
PR 18-SEP-2000; 2000US-233152P.
XX
PR 21-SEP-2000; 2000US-234140P.
XX
PR 13-FEB-2001; 2001US-268499P.
XX
PR 14-AUG-2001; 2001US-312185P.
XX
PA (BIOJ) BIOGEN INC.
XX
PI Ambrose CM, Thompson JS;
XX
XX WPI; 2002-362428/39.
DR N-PSDB; AAD35410.
XX
XX New human BAFF receptor proteins and nucleic acids, useful for
PT treating, preventing or delaying e.g. autoimmune diseases, cancers,
PT inherited genetic disorders involving B-cells, cardiovascular
PT disorders, or renal disorders
XX
PS Example 3; Fig 3; 164pp; English.

Query Match 98.8%; Score 954.5; DB 23; Length 266;
Best Local Similarity 99.5%; Pred. No. 1.1e-72;
Matches 184; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 MRGPRSLRGDRDAPATPCVPAECFOLLVHVCVACGLLTPRPKPXAGASSPAPRTALQP 60
Db 83 MRGPRSLRGDRDAPATPCVPAECFOLLVHVCVACGLLTPRPKPXAGASSPAPRTALQP 141
QY 61 QSVAGAGAGEAALPLPGLLFGAPALLGLALVLVGLVSWRRQRRLRGASSAEAPDG 120
Db 142 QSVAGAGAGEAALPLPGLLFGAPALLGLALVLVGLVSWRRQRRLRGASSAEAPDG 201
QY 121 DKDAPELDKVIILSPGISDATAPAMPPEGPCTTPPGHVSVPVPAELGSELVTTKTA 180
Db 202 DKDAPELDKVIILSPGISDATAPAMPPEGPCTTPPGHVSVPVPAELGSELVTTKTA 261
QY 181 GPEEQ 185
Db 262 GPEEQ 266

RESULT 6
AAE22270
ID AAE22270 standard; Protein; 185 AA.
XX
AC AAE22270;
XX
DT 25-JUL-2002 (first entry)
XX
DE Human BAFF receptor (BAFF-R) mutant, V20N.
XX
KW Human; BAFF receptor; BAFF-R; cytostatic; hypotensive; inflammation; TNF;
KW Tumour Necrosis Factor; autoimmune disease; immunosuppressive; cancer;
KW Myasthenia gravis; hypertension; organ transplantation; drug screening;
KW HIV; human immunodeficiency virus; genetic disorder; cardiovascular;
KW renal; rheumatoid arthritis; systemic lupus erythematosus; amyloidosis;
KW haemolytic anaemia; Chagas' disease; Grave's disease; glomerulonephritis;
KW multiple myeloma; chromosomal mapping; tissue typing; drug screening;
mutant; mutein.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX Misc-difference 20 /note= "Wild type Val substituted with Asn"
FT
FT
XX
XX WO200224909-A2.
XX
XX 28-MAR-2002.
XX
XX 06-SEP-2001; 2001WO-US28006.
XX
XX 18-SEP-2000; 2000US-233152P.

The invention relates to human BAFF receptor (BAFF-R) nucleic acids and proteins. BAFF-R is a B-cell activating factor belonging to the Tumour Necrosis Factor (TNF) family, which is associated with the expression of B-cells and immunoglobulins. The BAFF-R proteins, DNA and antibodies are useful for treating, preventing or delaying autoimmune diseases, cancer, tumorigenic conditions or inherited genetic disorders involving B-cells, hypertension, cardiovascular disorders, immunosuppressive diseases, renal

PR 21-SEP-2000; 2000US-234140P.
 PR 13-FEB-2001; 2001US-268499P.
 PR 14-AUG-2001; 2001US-312185P.
 XX (BIOJ) BIOGEN INC.
 XX Ambrose CM, Thompson JS;
 PI WPI; 2002-362428/39.
 DR New human BAFF receptor proteins and nucleic acids, useful for
 PT treating, preventing or delaying e.g. autoimmune diseases, cancers,
 PT inherited genetic disorders involving B-cells, cardiovascular
 PT disorders, or renal disorders
 XX
 XX Example 17; Page -; 164pp; English.
 XX The invention relates to human BAFF receptor (BAFF-R) nucleic acids and
 CC proteins. BAFF-R is a B-cell activating factor belonging to the tumour
 CC Necrosis Factor (TNF) family, which is associated with the expression of
 CC B-cells and immunoglobulins. The BAFF-R proteins, DNA and antibodies are
 CC useful for treating, preventing or delaying autoimmune diseases, cancer,
 CC tumorigenic conditions or inherited genetic disorders involving B-cells,
 CC hypertension, cardiovascular disorders, immunosuppressive diseases, renal
 CC disorders, inflammation, organ transplantation and HIV. Autoimmune
 CC diseases, which can be treated or prevented by BAFF-R, include systemic
 CC lupus erythematosus, rheumatoid arthritis, myasthenia gravis, autoimmune
 CC haemolytic anaemia, idiopathic thrombocytopenia purpura, Chagas' disease
 CC Grave's disease, anti-phospholipid syndrome, Wegener's granulomatosis,
 CC poly-arthritis nodosa and rapidly progressive glomerulonephritis. Plasma
 CC cells disorders e.g., multiple myeloma, Waldenström's macroglobulinaemia,
 CC heavy-chain disease, primary or immunocyte-associated amyloidosis, and
 CC monoclonal gammopathy of undetermined significance. The nucleic acid,
 CC protein, protein homologues, and antibodies may further be used in
 CC screening assays, in detection assays (chromosomal mapping, tissue typing
 CC or forensic biology), predictive medicine (e.g. diagnostic or prognostic
 CC assays, monitoring clinical trials, or pharmacogenomic). The polypeptides
 CC are further useful as immunogens to raise anti-BPFR antibodies, or in
 CC screening drugs or compounds that modulate BAFF-R activity or expression.
 CC The present sequence is human BAFF-R protein mutant.
 CC Note: The present sequence is not shown in the specification but is
 CC derived from human BAFF-R referred as SEQ ID NO: 5 (AAE22242) and shown
 CC in fig 2d of the specification.
 XX
 SQ Sequence 185 AA;
 Query Match 98.1%; Score 948; DB 23; Length 185;
 Best Local Similarity 97.8%; Pred. No. 2.7e-72;
 Matches 181; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 MRGGPSLRGRDAPPTPCVPAECFDLLVRHCACGLLRTPRXPXAGASSPAPRTALQP 60
 Db 1 MRGGPSLRGRDAPPTPCVPAECFDLLVRHCACGLLRTPRXPXAGASSPAPRTALQP 60
 QY 61 QSVGAGAGEAALPLGGLFGAPALLGLALVLVLGVSRRQRRLRGASSAEPDG 120
 Db 61 QSVGAGAGEAALPLGGLFGAPALLGLALVLVLGVSRRQRRLRGASSAEPDG 120
 QY 121 DXDAPPLDKVILSGISDATAPAMPPEPDGPTTPGHSVPVPATLSTELVTTKTA 180
 Db 121 DXDAPPLDKVILSGISDATAPAMPPEPDGPTTPGHSVPVPATLSTELVTTKTA 180
 QY 181 GPEQQ 185
 Db 181 GPEQQ 185

RESULT 7

AAE22271

ID AAE22271 standard; Protein; 185 AA.

XX

AC

XX

DT 25-JUL-2002 (first entry)
 XX Human BAFF receptor (BAFF-R) mutant, P21Q.
 DE
 XX Human; BAFF receptor; BAFF-R; cytostatic; hypotensive; inflammation; TNF;
 KW Tumour Necrosis Factor; autoimmune disease; immunosuppressive; cancer;
 KW myasthenia gravis; hypertension; organ transplantation; drug screening;
 KW HIV; human immunodeficiency virus; genetic disorder; cardiovascular;
 KW renal; rheumatoid arthritis; systemic lupus erythematosus; amyloidosis;
 KW haemolytic anaemia; Chagas' disease; Grave's disease; glomerulonephritis;
 KW multiple myeloma; chromosomal mapping; tissue typing; drug screening;
 KW mutant; muten.
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH Misc-difference 21 /note= "Wild type Pro substituted with Gln"
 FT WO200224909-A2.
 FN 28-MAR-2002.
 PD 06-SEP-2001; 2001WO-US28006.
 PF 18-SEP-2000; 2000US-233152P.
 XX 21-SEP-2000; 2000US-234140P.
 PR 13-FEB-2001; 2001US-268499P.
 PR 14-AUG-2001; 2001US-312185P.
 XX (BIOJ) BIOGEN INC.
 PA Ambrose CM, Thompson JS;
 PI WPI; 2002-362428/39.
 DR New human BAFF receptor proteins and nucleic acids, useful for
 PT treating, preventing or delaying e.g. autoimmune diseases, cancers,
 PT inherited genetic disorders involving B-cells, cardiovascular
 PT disorders, or renal disorders
 XX
 XX Example 17; Page -; 164pp; English.
 PS The invention relates to human BAFF receptor (BAFF-R) nucleic acids and
 CC proteins. BAFF-R is a B-cell activating factor belonging to the Tumour
 CC Necrosis Factor (TNF) family, which is associated with the expression of
 CC B-cells and immunoglobulins. The BAFF-R proteins, DNA and antibodies are
 CC useful for treating, preventing or delaying autoimmune diseases, cancer,
 CC tumorigenic conditions or inherited genetic disorders involving B-cells,
 CC hypertension, cardiovascular disorders, immunosuppressive diseases, renal
 CC disorders, inflammation, organ transplantation and HIV. Autoimmune
 CC diseases, which can be treated or prevented by BAFF-R, include systemic
 CC lupus erythematosus, rheumatoid arthritis, myasthenia gravis, autoimmune
 CC haemolytic anaemia, idiopathic thrombocytopenia purpura, Chagas' disease
 CC Grave's disease, anti-phospholipid syndrome, Wegener's granulomatosis,
 CC poly-arthritis nodosa and rapidly progressive glomerulonephritis. Plasma
 CC cells disorders e.g., multiple myeloma, Waldenström's macroglobulinaemia,
 CC heavy-chain disease, primary or immunocyte-associated amyloidosis, and
 CC monoclonal gammopathy of undetermined significance. The nucleic acid,
 CC protein, protein homologues, and antibodies may further be used in
 CC screening assays, in detection assays (chromosomal mapping, tissue typing
 CC or forensic biology), predictive medicine (e.g. diagnostic or prognostic
 CC assays, monitoring clinical trials, or pharmacogenomic). The polypeptides
 CC are further useful as immunogens to raise anti-BPFR antibodies, or in
 CC screening drugs or compounds that modulate BAFF-R activity or expression.
 CC The present sequence is human BAFF-R protein mutant.
 CC Note: The present sequence is not shown in the specification but is
 CC derived from human BAFF-R referred as SEQ ID NO: 5 (AAE22242) and shown
 CC in fig 2d of the specification.
 XX
 SQ Sequence 185 AA;
 Query Match 98.0%; Score 947; DB 23; Length 185;

Best Local Similarity 97.8%; Pred. No. 3.3e-72;
Matches 181; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MRRGPRSLRGDAPAPPCVPACSCFLLVHVCACGLLTPRPKPXAGASSPAPRTALQP 60
DB 1 MRRGPRSLRGDAPAPPCVPQVQACSCFLLVHVCACGLLTPRPKPAGASSPAPRTALQP 60
QY 61 QESVAGAGAEALPLPGLLFGAPALLGLALVLAIVLGVSVRRRQRLRGASSAEAPDG 120
DB 61 QESVAGAGAEALPLPGLLFGAPALLGLALVLAIVLGVSVRRRQRLRGASSAEAPDG 120
QY 121 DKDAPEPLDKVILSPGISDATAPAPPPGDDPTTPPGHVSVPVPA TELGSELVTTKTA 180
DB 121 DKDAPEPLDKVILSPGISDATAPAPPPGDDPTTPPGHVSVPVPA TELGSELVTTKTA 180
QY 181 GPEQ 185
DB 181 GPEQ 185

RESULT 8
AAE22268
ID AAE22268 standard; Protein; 185 AA.
XX
AC AAE22268;
XX
DT 25-JUL-2002 (first entry)
XX
DE Human BAFF receptor (BAFF-R) mutant, V20N/A22T.
XX
KW Human; BAFF receptor; BAFF-R; cytostatic; hypotensive; inflammation; TNF;
KW Tumour Necrosis Factor; autoimmune disease; immunosuppressive; cancer;
KW myasthenia gravis; hypertension; organ transplantation; drug screening;
KW HIV; human immunodeficiency virus; genetic disorder; cardiovascular;
KW renal; rheumatoid arthritis; systemic lupus erythematosus; amyloidosis;
KW haemolytic anaemia; Chagas' disease; Grave's disease; glomerulonephritis;
KW multiple myeloma; chromosomal mapping; tissue typing; drug screening;
KW mutant; mutein.
XX
OS Homo sapiens.
XX
XX
XX
FH Key Location/Qualifiers
FT Misc-difference 20 /note= "Wild type Val substituted with Asn"
FT Misc-difference 22 /note= "Wild type Ala substituted with Thr"
XX
XX
PN WO200224909-A2.
XX
PD 28-MAR-2002.
XX
XX
XX 06-SEP-2001; 2001WO-28006.
XX
XX 18-SEP-2000; 2000US-233152P.
PR 21-SEP-2000; 2000US-234140P.
PR 13-FEB-2001; 2001US-268499P.
PR 14-AUG-2001; 2001US-312185P.
XX
XX (BIOJ) BIOGEN INC.
XX
XX Ambrose CM, Thompson JS;
XX
XX WPI, 2002-362428/39.
XX
XX New human BAFF receptor proteins and nucleic acids, useful for
PT treating, preventing or delaying e.g. autoimmune diseases, cancers,
PT inherited genetic disorders involving B-cells, cardiovascular
PT disorders, or renal disorders -
XX
XX Example 17; Page -; 164pp; English.
XX
XX The invention relates to human BAFF receptor (BAFF-R) nucleic acids and
CC proteins. BAFF-R is a B-cell activating factor belonging to the Tumour

CC Necrosis Factor (TNF) family, which is associated with the expression of
CC B-cells and immunoglobulins. The BAFF-R proteins, DNA and antibodies are
CC useful for treating, preventing or delaying autoimmune diseases, cancer,
CC tumorigenic conditions or inherited genetic disorders involving B-cells,
CC hypertension, cardiovascular disorders, immunosuppressive diseases, renal
CC disorders, inflammation, organ transplantation and HIV. Autoimmune
CC diseases, which can be treated or prevented by BAFF-R, include systemic
CC lupus erythematosus, rheumatoid arthritis, myasthenia gravis, Chagas' disease
CC haemolytic anaemia, idiopathic thrombocytopenia purpura, Wegener's disease
CC Grave's disease, anti-phospholipid syndrome, Wegener's granulomatosis,
CC poly-arthritis nodosa and rapidly progressive glomerulonephritis. Plasma
CC cells disorders e.g., multiple myeloma, Waldenstrom's macroglobulinaemia,
CC heavy-chain disease, primary or immunocyte-associated amyloidosis, and
CC monoclonal gammopathy of undetermined significance. The nucleic acids,
CC protein, protein homologues, and antibodies may further be used in
CC screening assays, in detection assays (chromosomal mapping, tissue typing
CC or forensic biology), predictive medicine (e.g. diagnostic or prognostic
CC assays, monitoring clinical trials, or pharmacogenomic). The polypeptides
CC are further useful as immunogens to raise anti-BAFF-R antibodies, or in
CC screening drugs or compounds that modulate BAFF-R activity or expression.
CC The present sequence is human BAFF-R protein mutant.
CC Note: The present sequence is not shown in the specification but is
CC derived from human BAFF-R referred as SEQ ID NO: 5 (AAE22242) and shown
CC in fig 2d of the specification.

XX
SQ Sequence 185 AA;

Query Match 97.7%; Score 944; DB 23; Length 185;
Best Local Similarity 97.3%; Pred. No. 5.9e-72;
Matches 180; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 MRRGPRSLRGDAPAPPCVPACSCFLLVHVCACGLLTPRPKPXAGASSPAPRTALQP 60
DB 1 MRRGPRSLRGDAPAPPCVPQVQACSCFLLVHVCACGLLTPRPKPAGASSPAPRTALQP 60
QY 61 QESVAGAGAEALPLPGLLFGAPALLGLALVLAIVLGVSVRRRQRLRGASSAEAPDG 120
DB 61 QESVAGAGAEALPLPGLLFGAPALLGLALVLAIVLGVSVRRRQRLRGASSAEAPDG 120
QY 121 DKDAPEPLDKVILSPGISDATAPAPPPGDDPTTPPGHVSVPVPA TELGSELVTTKTA 180
DB 121 DKDAPEPLDKVILSPGISDATAPAPPPGDDPTTPPGHVSVPVPA TELGSELVTTKTA 180
QY 181 GPEQ 185
DB 181 GPEQ 185

RESULT 9
AAE22269
ID AAE22269 standard; Protein; 185 AA.
XX
AC AAE22269;
XX
DT 25-JUL-2002 (first entry)
XX
XX Human BAFF receptor (BAFF-R) mutant, V20N/P21Q.

Human; BAFF receptor; BAFF-R; cytostatic; hypotensive; inflammation; TNF;
KW Tumour Necrosis Factor; autoimmune disease; immunosuppressive; cancer;
KW myasthenia gravis; hypertension; organ transplantation; drug screening;
KW HIV; human immunodeficiency virus; genetic disorder; cardiovascular;
KW renal; rheumatoid arthritis; systemic lupus erythematosus; amyloidosis;
KW haemolytic anaemia; Chagas' disease; Grave's disease; glomerulonephritis;
KW multiple myeloma; chromosomal mapping; tissue typing; drug screening;
KW mutant; mutein.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FT Misc-difference 20 /note= "Wild type Val substituted with Asn"
FT Misc-difference 21

PT FT /note= "Wild type Pro substituted with Gln"

XX PN WO200224909-A2.

XX PD 28-MAR-2002.

XX PF 06-SEP-2001; 2001WO-US28006.

XX PR 18-SEP-2000; 2000US-233152P.

XX PR 21-SEP-2000; 2000US-234140P.

XX PR 13-FEB-2001; 2001US-268499P.

XX PR 14-AUG-2001; 2001US-312185P.

XX PA (BIOJ) BIOGEN INC.

XX PI Ambrose CM, Thompson JS;

XX PI WPI; 2002-362428/39.

XX DR New human BAFF receptor proteins and nucleic acids, useful for

XX PT treating, preventing or delaying e.g. autoimmune diseases, cancers,

XX PT inherited genetic disorders involving B-cells, cardiovascular

XX PT disorders, or renal disorders

XX PS Example 17; Page -; 164pp; English.

XX CC The invention relates to human BAFF receptor (BAFF-R) nucleic acids and

XX CC proteins. BAFF-R is a B-cell activating factor belonging to the Tumour

XX CC Necrosis Factor (TNF) family, which is associated with the expression of

XX CC B-cells and immunoglobulins. The BAFF-R proteins, DNA and antibodies are

XX CC useful for treating, preventing or delaying autoimmune diseases, cancer,

XX CC tumourigenic conditions or inherited genetic disorders involving B-cells,

XX CC hypertension, cardiovascular disorders, immunosuppressive diseases, renal

XX CC disorders, inflammation, organ transplantation and HIV. Autoimmune

XX CC diseases, which can be treated or prevented by BAFF-R, include systemic

XX CC lupus erythematosus, rheumatoid arthritis, myasthenia gravis, autoimmune

XX CC Grave's disease, idiopathic thrombocytopenia purpura, Chagas' disease

XX CC haemolytic anaemia, idiopathic thrombocytopenia purpura, Chagas' disease

XX CC poly-arthritis nodosa and rapidly progressive glomerulonephritis. Plasma

XX CC cells disorders e.g., multiple myeloma, Waldenstrom's macroglobulinaemia,

XX CC heavy-chain disease, primary or immunocyte-associated amyloidosis, and

XX CC monoclonal gammopathy of undetermined significance. The nucleic acids,

XX CC protein, protein homologues, and antibodies may further be used in

XX CC screening assays, in detection assays (chromosomal mapping, tissue typing

XX CC or forensic biology), predictive medicine (e.g. diagnostic or prognostic

XX CC assays, monitoring clinical trials, or pharmacogenomic). The polypeptides

XX CC are further useful as immunogens to raise anti-BAFF antibodies, or in

XX CC screening drugs or compounds that modulate BAFF-R activity or expression.

XX CC The present sequence is human BAFF-R protein mutant.

XX CC Note: The present sequence is not shown in the specification but is

XX CC derived from human BAFF-R referred as SEQ ID NO: 5 (AAE22242) and shown

XX CC in fig 2d of the specification.

XX SQ Sequence 185 AA;

Query Match 97.3%; Score 940; DB 23; Length 185;

Best Local Similarity 97.3%; Pred. No. 1.3e-71;

Matches 180; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 MRGRPSLRGRDAPATPCVPACDFLLVHVCAGLLTRPKPKXAGASSPAPRTALQP 60

DB 1 MRGRPSLRGRDAPATPCVQACDFLLVHVCAGLLTRPKPKXAGASSPAPRTALQP 60

QY 61 QESVGAGAGBAALPLPGLLFGAPALLGLALVALVLVGLVSRQRRLRGASSAEPDG 120

DB 61 QESVGAGAGBAALPLPGLLFGAPALLGLALVALVLVGLVSRQRRLRGASSAEPDG 120

QY 121 DKDAPEPLDKVILSPGISDATAPAMPPEGDPGTTPGCHSVVPVATLGSTELVTYKTA 180

DB 121 DKDAPEPLDKVILSPGISDATAPAMPPEGDPGTTPGCHSVVPVATLGSTELVTYKTA 180

QY 181 GPEQQ 185

|||||

DB 181 GPEQQ 185

RESULT 10

AAE22267

ID AAE22267 standard; Protein; 185 AA.

AC AAE22267;

XX 25-JUL-2002 (first entry)

XX Human BAFF receptor (BAFF-R) mutant, V20N/P21Q/A22T.

XX Human; BAFF receptor; BAFF-R; cytostatic; hypotensive; inflammation; TNF;

XX Tumour Necrosis Factor; autoimmune disease; immunosuppressive; cancer;

XX myasthenia gravis; hypertension; organ transplantation; drug screening;

XX HIV; human immunodeficiency virus; genetic disorder; cardiovascular;

XX renal; rheumatoid arthritis; systemic lupus erythematosus; amyloidosis;

XX haemolytic anaemia; Chagas' disease; Grave's disease; glomerulonephritis;

XX multiple myeloma; chromosomal mapping; tissue typing; drug screening;

XX mutant; mutein.

XX Homo sapiens.

XX Key Location/Qualifiers

XX FT Misc-difference 20 /note= "Wild type Val substituted with Asn"

XX FT Misc-difference 21 /note= "Wild type Pro substituted with Gln"

XX FT Misc-difference 22 /note= "Wild type Ala substituted with Thr"

XX WO200224909-A2.

XX 28-MAR-2002.

XX 06-SEP-2001; 2001WO-US28006.

XX 18-SEP-2000; 2000US-233152P.

XX 21-SEP-2000; 2000US-234140P.

XX 13-FEB-2001; 2001US-268499P.

XX 14-AUG-2001; 2001US-312185P.

XX (BIOJ) BIOGEN INC.

XX Ambrose CM, Thompson JS;

XX WPI; 2002-362428/39.

XX New human BAFF receptor proteins and nucleic acids, useful for

XX PT treating, preventing or delaying e.g. autoimmune diseases, cancers,

XX PT inherited genetic disorders involving B-cells, cardiovascular

XX PT disorders, or renal disorders

XX Example 17; Page -; 164pp; English.

XX The invention relates to human BAFF receptor (BAFF-R) nucleic acids and

XX CC proteins. BAFF-R is a B-cell activating factor belonging to the Tumour

XX CC Necrosis Factor (TNF) family, which is associated with the expression of

XX CC B-cells and immunoglobulins. The BAFF-R proteins, DNA and antibodies are

XX CC useful for treating, preventing or delaying autoimmune diseases, cancer,

XX CC tumourigenic conditions or inherited genetic disorders involving B-cells,

XX CC hypertension, cardiovascular disorders, immunosuppressive diseases, renal

XX CC disorders, inflammation, organ transplantation and HIV. Autoimmune

XX CC diseases, which can be treated or prevented by BAFF-R, include systemic

XX CC lupus erythematosus, rheumatoid arthritis, myasthenia gravis, autoimmune

XX CC haemolytic anaemia, idiopathic thrombocytopenia purpura, Chagas' disease

XX CC Grave's disease, anti-phospholipid syndrome, Wegener's granulomatosis,

XX CC poly-arthritis nodosa and rapidly progressive glomerulonephritis. Plasma

XX CC cells disorders e.g., multiple myeloma, Waldenstrom's macroglobulinaemia,

XX CC heavy-chain disease, primary or immunocyte-associated amyloidosis, and

XX CC monoclonal gammopathy of undetermined significance. The nucleic acids,

XX CC protein, protein homologues, and antibodies may further be used in

screening assays, in detection assays (chromosomal mapping, tissue typing or forensic biology), predictive medicine (e.g. diagnostic or prognostic assays, monitoring clinical trials, or pharmacogenomic). The polypeptides are further useful as immunogens to raise anti-BFR antibodies, or in screening drugs or compounds that modulate BFR activity or expression. The present sequence is human BFR protein mutant.
Note: The present sequence is not shown in the specification but is derived from human BFR-R referred as SEQ ID NO: 5 (AAE22242) and shown in fig 2d of the specification.

XX SQ Sequence 185 AA;
Query Match 96.9%; Score 936; DB 23; Length 185;
Best Local Similarity 96.8%; Pred. No. 2.8e-71;
Matches 179; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 MRGPRSLRGDAPAPPCVPACFDLLVVRHCACGLLTPRPKXAGASSPAPRTALQP 60
DB 1 MRGPRSLRGDAPAPPCVQTCFLLVVRHCACGLLTPRPKXAGASSPAPRTALQP 60
QY 61 QESVGAGAGEAALPLGGLFGAPALLGLALVLVLVGLVSWRRQRRLRGASSAEAPDG 120
DB 61 QESVGAGAGEAALPLGGLFGAPALLGLALVLVLVGLVSWRRQRRLRGASSAEAPDG 120
QY 121 DKDAPEPLDKVILSPGISDATAPAWPPGDDPTTPGHSVPVPA TELGTELVTTKTA 180
DB 121 DKDAPEPLDKVILSPGISDATAPAWPPGDDPTTPGHSVPVPA TELGTELVTTKTA 180
QY 181 GPEQQ 185
DB 181 GPEQQ 185

RESULT 11

ID AAE22266 standard; Protein; 185 AA.
XX AC AAE22266;
XX 25-JUL-2002 (first entry)
XX Human BFR receptor (BFR-R) mutant, V20N/P21Q/A22T/L27P.
XX Human; BFR receptor; BFR-R; cytostatic; hypotensive; inflammation; TNF;
KW Tumour Necrosis Factor; autoimmune disease; immunosuppressive; cancer;
KW Myasthenia Gravis; hypertension; organ transplantation; drug screening;
KW HIV; human immunodeficiency virus; genetic disorder; cardiovascular;
KW renal; rheumatoid arthritis; systemic lupus erythematosus; amyloidosis;
KW haemolytic anaemia; Chagas' disease; Grave's disease; glomerulonephritis;
KW multiple myeloma; chromosomal mapping; tissue typing; drug screening;
KW mutant; mutein.
XX Homo sapiens.
OS
EH Key Location/Qualifiers
FT Misc-difference 20 /note= "Wild type Val substituted with Asn"
FT Misc-difference 21 /note= "Wild type Pro substituted with Gln"
FT Misc-difference 22 /note= "Wild type Ala substituted with Thr"
FT Misc-difference 27 /note= "Wild type Leu substituted with Pro"
XX WO200224909-A2.
XX 28-MAR-2002.
XX 06-SEP-2001; 2001WO-US28006.
XX 18-SEP-2000; 2000US-233152P.
XX 21-SEP-2000; 2000US-234140P.
XX 13-FEB-2001; 2001US-268499P.
PR

PR 14-AUG-2001; 2001US-312185P.
XX (BIOJ) BIOGEN INC.
XX Ambrose CM, Thompson JS;
XX WFI; 2002-362428/39.
XX New human BFR receptor proteins and nucleic acids, useful for treating, preventing or delaying e.g. autoimmune diseases, cancers, inherited genetic disorders involving B-cells, cardiovascular disorders, or renal disorders -
XX Example 17; Page -; 164pp; English.
XX The invention relates to human BFR receptor (BFR-R) nucleic acids and proteins. BFR-R is a B-cell activating factor belonging to the Tumour Necrosis Factor (TNF) family, which is associated with the expression of B-cells and immunoglobulins. The BFR-R proteins, DNA and antibodies are useful for treating, preventing or delaying autoimmune diseases, cancer, tumourigenic conditions or inherited genetic disorders involving B-cells, hypertension, cardiovascular disorders, immunosuppressive diseases, renal disorders, inflammation, organ transplantation and HIV. Autoimmune diseases, which can be created or prevented by BFR-R, include systemic lupus erythematosus, rheumatoid arthritis, myasthenia gravis, autoimmune haemolytic anaemia, idiopathic thrombocytopenia purpura, Chagas' disease, Grave's disease, anti-phospholipid syndrome, Wegener's granulomatosis, poly-arthritis nodosa and rapidly progressive glomerulonephritis. Plasma cells disorders e.g., multiple myeloma, Waldenstrom's macroglobulinaemia, heavy-chain disease, primary or immunocyte-associated amyloidosis, and monoclonal gammopathy of undetermined significance. The nucleic acids, protein, protein homologues, and antibodies may further be used in screening assays, in detection assays (chromosomal mapping, tissue typing or forensic biology), predictive medicine (e.g. diagnostic or prognostic assays, monitoring clinical trials, or pharmacogenomic). The polypeptides are further useful as immunogens to raise anti-BFR antibodies, or in screening drugs or compounds that modulate BFR-R activity or expression. The present sequence is human BFR-R protein mutant.
Note: The present sequence is not shown in the specification but is derived from human BFR-R referred as SEQ ID NO: 5 (AAE22242) and shown in fig 2d of the specification.

XX SQ Sequence 185 AA;

Query Match 96.2%; Score 929; DB 23; Length 185;
Best Local Similarity 96.2%; Pred. No. 1.1e-70;
Matches 178; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 1 MRGPRSLRGDAPAPPCVPACFDLLVVRHCACGLLTPRPKXAGASSPAPRTALQP 60
DB 1 MRGPRSLRGDAPAPPCVQTCFLLVVRHCACGLLTPRPKXAGASSPAPRTALQP 60
QY 61 QESVGAGAGEAALPLGGLFGAPALLGLALVLVLVGLVSWRRQRRLRGASSAEAPDG 120
DB 61 QESVGAGAGEAALPLGGLFGAPALLGLALVLVLVGLVSWRRQRRLRGASSAEAPDG 120
QY 121 DKDAPEPLDKVILSPGISDATAPAWPPGDDPTTPGHSVPVPA TELGTELVTTKTA 180
DB 121 DKDAPEPLDKVILSPGISDATAPAWPPGDDPTTPGHSVPVPA TELGTELVTTKTA 180
QY 181 GPEQQ 185
DB 181 GPEQQ 185

RESULT 12
ABB78398
ID ABB78398 standard; Protein; 175 AA.
XX ABB78398;
XX AC ABB78398;
XX 17-DEC-2002 (first entry)
XX

DE Amino acid sequence of murine TRAF3-binding B cell-specific receptor.
XX Mouse; TRAF3-binding B cell-specific receptor; TRAF3;
KW signal transduction; TNF ligand; cancer; autoimmune disease; apoplexia;
KW viral infection; AIDS; bone disease; transplantation rejection;
KW Alzheimer's disease; ischaemia; rheumatoid arthritis; cachexia.
XX
OS Mus sp.
XX WO200272827-A1.
XX 19-SEP-2002.
XX 28-FEB-2002; 2002WO-JP01849.
XX 28-FEB-2001; 2001JP-0055119.
XX (RIKE) RIKEN KK.
PA (IRIE/) IRIE S.
PA (SATO/) SATO T.
XX
PI Irie S, Sato T;
XX
XX WPI; 2002-713516/77.
DR N-PSDB; ABV72373.
XX
XX TRAF3-binding B cell-specific receptor and encoded gene, applicable in
PT diagnosis of abnormality due to TRAF3-mediated intracellular signal
PT transduction and in screening drugs for e.g. cancer, autoimmune
PT diseases and AIDS -
XX
XX Claim 1; Page 47-48; 57pp; Japanese.
XX
XX The present sequence represents a murine TRAF3-binding B cell-specific
CC receptor. The polynucleotide and polypeptide sequence of this receptor
CC are useful for diagnosis of abnormality due to TRAF3-mediated
CC intracellular signal transduction and in screening drugs for diseases
CC associated with TNF ligand family and TNF receptor-ligand superfamily
CC e.g. cancer, autoimmune diseases, viral infections like AIDS, bone
CC diseases, transplantation rejection, Alzheimer's disease, ischaemia,
CC rheumatoid arthritis, apoplexia and cachexia.
XX
XX Sequence 175 AA;
XX
XX Query Match 42.5%; Score 411; DB 23; Length 175;
XX Best Local Similarity 55.8%; Pred. No. 4.9e-27;
XX Matches 101; Conservative 9; Mismatches 55; Indels 16; Gaps 6;
QY 6 RSLRGDAPATPCVPACFCDFLLVHCACGLLTPRPKPVAGASSPAPRTALQPOESVG 65
Db 9 RSQRSDSSVPTQCNQTECFDPLVNCVSCLEFHTP---DTGHTSSLEPGTALQPOB--- 62
QY 66 AGAGEAALPLPGLLFGAPALLGLALVLAIV-LVGLVSWRRQRRLRGASSAEPDGKDA 124
Db 63 ---GSALRPDVALVLCAPALLGLLALTLVGLVLSVSWRWQ-QLRTAS-----PDTSEGV 114
QY 125 -PFLPKVILSPGSDATAPAWPPGPDGTPTPGHVSVPVPA TELGSLVTTKTAGPE 163
Db 115 QQSLENVFPSSSETPHASAPTWPKEDADSDALPRHSVPVPATELGSLVTTKTAGPE 174
QY 184 Q 184
Db 175 Q 175

RESULT 13
ABBS1489
ID ABB81489 standard; Protein; 175 AA.
AC ABB81489;
XX
XX 02-SEP-2002 (first entry)
DT
XX

DE Mouse Ztnfr12 protein SEQ ID NO:13.
XX Human; Ztnfr12; tumour necrosis factor receptor; cytostatic;
XX immunosuppressive; dermatological; antiinflammatory; antidiabetic;
KW neuroprotective; antirheumatic; antiarthritic; antiasthmatic;
KW nephrotropic; hypotensive; gene therapy; B lymphocyte; tumour;
KW autoimmune disorder; systemic lupus erythematosus; myasthenia gravis;
KW multiple sclerosis; insulin dependent diabetes mellitus; asthma;
KW rheumatoid arthritis; bronchitis; emphysema; renal disease; lymphoma;
KW glomerulonephritis; vasculitis; chronic lymphoid leukaemia; nephritis;
KW pyelonephritis; renal neoplasm; multiple myeloma; amyloidosis;
KW light chain neuropathy; hypertension; large vessel disease;
KW graft-versus host disease; graft rejection; Crohn's disease.
XX
XX Mus sp.
XX WO200238766-A2.
XX 16-MAY-2002.
XX 05-NOV-2001; 2001WO-US47018.
XX 07-NOV-2000; 2000US-246449P.
XX 20-DEC-2000; 2000US-257131P.
XX 28-JUN-2001; 2001US-301715P.
XX 29-AUG-2001; 2001US-315565P.
XX (ZYMO) ZYMOGENETICS INC.
XX Gross JA, Xu W, Henne RM, Grant FJ;
PI WPI; 2002-508212/54.
XX N-PSDB; AEN89431.
XX
XX Novel isolated human tumor necrosis factor receptor polypeptide, termed
PT Ztnfr 12, useful for treating autoimmune disorders, emphysema, end
PT stage renal failure or renal disease and lymphoma -
XX
XX Disclosure; Page 140; 154pp; English.
XX
XX The present invention describes a human tumour necrosis factor receptor
CC designated Ztnfr12 (I). (I) has cytostatic, immunosuppressive,
CC dermatological, antiinflammatory, neuroprotective, antidiabetic,
CC antirheumatic, antiarthritic, antiasthmatic, nephrotropic and hypotensive
CC activities, and can be used in gene therapy. (I) can be used for
CC inhibiting, in a mammal, the activity of a ligand that binds Ztnfr12
CC (e.g. ZTNF4), for treating disorders and diseases associated with B
CC lymphocytes, activated B lymphocytes or resting B lymphocytes, and for
CC inhibiting the proliferation of tumour cells. (I) is useful for treating
CC autoimmune disorders such as systemic lupus erythematosus, myasthenia
CC gravis, multiple sclerosis, insulin dependent diabetes mellitus, asthma,
CC rheumatoid arthritis, bronchitis, emphysema and end stage renal failure
CC or renal disease such as glomerulonephritis, vasculitis, chronic lymphoid
CC leukaemia, nephritis, and pyelonephritis, and for treating renal
CC neoplasms, multiple myelomas, lymphomas, light chain neuropathy, or
CC amyloidosis, hypertension, large vessel diseases, graft-versus host
CC disease, graft rejection and Crohn's disease. (I) is useful for
CC modulating the immune system, for regulating B cell responses and
CC development, for modulating development of other cells, antibody
CC production and cytokine production, and for modulating T and B cell
CC communication. The present sequence represents mouse Ztnfr12 which is
CC given in the exemplification of the present invention.
XX
XX Sequence 175 AA;
XX

Query Match 42.5%; Score 411; DB 23; Length 175;
Best Local Similarity 55.8%; Pred. No. 4.9e-27;
Matches 101; Conservative 9; Mismatches 55; Indels 16; Gaps 6;

QY 6 RSLRGDAPATPCVPACFCDFLLVHCACGLLTPRPKPVAGASSPAPRTALQPOESVG 65
Db 9 RSQRSDSSVPTQCNQTECFDPLVNCVSCLEFHTP---DTGHTSSLEPGTALQPOB--- 62

QY 66 AGAGEAALPLPGLLFGAPALLGLALVIALV-LVGLVSWRRRRRLRGASSAEPDGDKDA 124
Db 63 ---GSALRPDVALVGPALLGLILALTIVGLVSLVSWWRQ-QLRTAS---PDTSEGV 114
QY 125 -PEPLDKVILSPGISDATAPAWPPGDPGTTTPGHSVPVPATELGSELVTTKTAGE 183
Db 115 QQSELENVFPVPSSETHASAPTPFLKEDASALPRHSVPVPATELGSELVTTKTAGE 174
QY 184 Q 184
Db 175 Q 175
RESULT 14
AAE22244
ID AAE22244 standard; Protein; 175 AA.
XX AC AAE22244;
XX DT 25-JUL-2002 (first entry)
XX DE Murine BAFF receptor (BAFF-R) protein.
XX KW Murine; BAFF receptor; BAFF-R; cytostatic; hypotensive; inflammation;
KW Tumour Necrosis Factor; autoimmune disease; immunosuppressive; cancer;
KW myasthenia gravis; hypertension; organ transplantation; drug screening;
KW HIV; human immunodeficiency virus; Genetic disorder; cardiovascular; TNF;
KW renal; rheumatoid arthritis; systemic lupus erythematosus; amyloidosis;
KW haemolytic anaemia; Chagas' disease; Grave's disease; glomerulonephritis;
KW multiple myeloma; chromosomal mapping; tissue typing; drug screening.
XX OS Mus musculus.
XX FH Key Location/Qualifiers
XX FT Domain 70..97
XX FT /label= Transmembrane_domain
XX PN WO200224909-A2.
XX PD 28-MAR-2002.
XX PF 06-SEP-2001; 2001WO-US28006.
XX PR 18-SEP-2000; 2000US-233152P.
XX PR 21-SEP-2000; 2000US-234140P.
XX PR 13-FEB-2001; 2001US-268499P.
XX PR 14-AUG-2001; 2001US-312185P.
XX PA (BIOJ) BIOGEN INC.
XX PI Ambrose CM, Thompson JS;
XX DR WPI; 2002-362428/39.
XX DR N-PSDB; AAD35411.
XX PT New human BAFF receptor proteins and nucleic acids, useful for
PT treating, preventing or delaying e.g. autoimmune diseases, cancers,
PT inherited genetic disorders involving B-cells, cardiovascular
PT disorders, or renal disorders
XX PS Example 4; Fig 4b; 164pp; English.
XX CC The invention relates to human BAFF receptor (BAFF-R) nucleic acids and
CC proteins. BAFF-R is a B-cell activating factor belonging to the Tumour
CC Necrosis Factor (TNF) family, which is associated with the expression of
CC B-cells and immunoglobulins. The BAFF-R proteins, DNA and antibodies are
CC useful for treating, preventing or delaying autoimmune diseases, cancer,
CC tumourigenic conditions or inherited genetic disorders involving B-cells,
CC hypertension, cardiovascular disorders, immunosuppressive diseases, renal
CC disorders, inflammation, organ transplantation and HIV. Autoimmune
CC diseases, which can be treated or prevented by BAFF-R, include systemic
CC lupus erythematosus, rheumatoid arthritis, myasthenia gravis, autoimmune
CC haemolytic anaemia, idiopathic thrombocytopenia purpura, Chagas' disease

CC Grave's disease, anti-phospholipid syndrome, Wegener's granulomatosis,
CC poly-arthritis nodosa and rapidly progressive glomerulonephritis. Plasma
CC cells disorders e.g., multiple myeloma, Waldenstrom's macroglobulinaemia,
CC heavy-chain disease, primary or immunocyte-associated amyloidosis, and
CC monoclonal gammopathy of undetermined significance. The nucleic acids,
CC protein, protein homologues, and antibodies may further be used in
CC screening assays, in detection assays (chromosomal mapping, tissue typing
CC or forensic biology), predictive medicine (e.g. diagnostic or prognostic
CC assays, monitoring clinical trials, or pharmacogenomic). The polypeptides
CC are further useful as immunogens to raise anti-BaFF antibodies, or in
CC screening drugs or compounds that modulate BAFF-R activity or expression.
XX CC The present sequence is murine BAFF-R protein.
XX SQ Sequence 175 AA;
Query Match 42.5%; Score 411; DB 23; Length 175;
Best Local Similarity 55.8%; Pred. No. 4.9e-27;
Matches 101; Conservative 9; Mismatches 55; Indels 16; Gaps 6;
QY 6 RSLRGDAPAPTEPCVPAECFDLLVHVCAGLLRTPRKPKXAGASSAPRITALQPOESVG 65
Db 9 RQSRSDSVPTQCNTQCFDPLVNCVSCLEFHTP---DTGHTSSLEPGTALQPE--- 62
QY 66 AGAGEAALPLPGLLFGAPALLGLALVIALV-LVGLVSWRRRRRLRGASSAEPDGDKDA 124
Db 63 ---GSALRPDVALVGPALLGLILALTIVGLVSLVSWWRQ-QLRTAS---PDTSEGV 114
QY 125 -PEPLDKVILSPGISDATAPAWPPGDPGTTTPGHSVPVPATELGSELVTTKTAGE 183
Db 115 QQSELENVFPVPSSETHASAPTPFLKEDASALPRHSVPVPATELGSELVTTKTAGE 174
QY 184 Q 184
Db 175 Q 175
RESULT 15
ABP97722
ID ABP97722 standard; Protein; 175 AA.
XX AC ABP97722;
XX DT 28-MAY-2003 (first entry)
XX DE Amino acid sequence of murine BR3 receptor.
XX KW Human; TAC1; BR3; receptor; tumour necrosis factor ligand; TNF ligand;
KW TALL-1; April; systemic lupus erythematosus.
XX OS Mus sp.
XX PN WO2003014294-A2.
XX PD 20-FEB-2003.
XX PF 24-JUL-2002; 2002WO-US23487.
XX PR 03-AUG-2001; 2001US-310114P.
XX PR 30-APR-2002; 2002US-377171P.
XX PA (GETH) GENENTECH INC.
XX PI Dixit V, Grewal I, Ridgway J, Yan M;
XX DR WPI; 2003-248010/25.
XX DR N-PSDB; AB68876.
XX PT New nucleic acid encoding a TAC1s or BR3 polypeptide, useful for
XX PT preparing a composition for treating systemic lupus erythematosus
XX PS Disclosure; Fig 9A; 153pp; English.
XX CC The present sequence represents a murine BR3 polypeptide. The

CC specification also describes TACI polypeptides. TACI and BR3 are
CC receptors. Tumour necrosis factor (TNF) family ligands TALL-1 and
CC April bind to the TACI receptor, while TNF family ligands TALL-1 also
CC binds to BR3 receptor. The TACI and BR3 receptor nucleic acid is useful
CC for preparing a composition for treating systemic lupus erythematosus.
XX
SQ Sequence 175 AA;
Query Match 42.5%; Score 411; DB 24; Length 175;
Best Local Similarity 55.8%; Pred. No. 4.9e-27;
Matches 101; Conservative 9; Mismatches 55; Indels 16; Gaps 6;
QY 6 RSLRGDAPAPTCVPAECFDLLVRHCVACGLLRTPRPKPXAGASSPAPRTALOPQESVG 65
DB 9 RSQSRDSSVPTQCNQTECFDPLVRNCVSCLELFTFP---DTGHTSSLFPGTALQPE--- 62
QY 66 AGAGEAALPLPGLLFGAPALLGLALVLAIV-LVGLVSWRRORRLRGASSAEAPDGDKDA 124
DB 63 ---GSALRPDVALLVGAPALLGLLALTLVGLVSLVSWRWQ-QLRTAS---PDTSEGV 114
QY 125 -PEPLDKVILSPGISDATAPAPPPGPDGTPPCHSVFVPEATELGSTELVTTKTAGPE 183
DB 115 QQESLENVFPSSETHAGAPTWPLPKEDADSPALPRHSVFPVPEATELGSTELVTTKTAGPE 174
QY 184 Q 184
DB 175 Q 175

Search completed: February 5, 2004, 17:59:01
Job time : 39.5417 secs

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OM protein - protein search, using sw model

Run on: February 5, 2004, 18:00:55 ; Search time 30.8333 Seconds
(without alignments)
1256.294 Million cell updates/sec

Title: US-10-045-574b-27

Perfect score: 966

Sequence: 1 MRRGRSLRGDAPPTFCV.....ATELGSTELVTTKTAGPEQ 185

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications AA:
- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
 - 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
 - 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
 - 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
 - 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
 - 6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
 - 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
 - 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
 - 9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
 - 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
 - 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
 - 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
 - 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
 - 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
 - 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
 - 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
 - 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
 - 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	954.5	98.8	184	15	US-10-008-063-2
2	954.5	98.8	184	15	US-10-152-363A-60
3	825.5	85.5	185	15	US-10-251-947-2
4	755.5	78.2	171	15	US-10-251-947-4
5	755.5	78.2	171	15	US-10-251-947-7
6	746	77.2	170	15	US-10-231-947-6
7	746	77.2	186	15	US-10-251-947-14
8	411	42.5	175	15	US-10-008-063-13
9	373.5	38.7	328	15	US-10-008-063-42
10	178	18.4	38	12	US-10-145-206-195
11	149	15.4	26	12	US-10-271-343-32
12	121	12.5	19652	12	US-10-084-846A-7
13	118	12.2	422	7	US-08-736-013-170
14	115	11.9	356	15	US-10-177-293-214
15	115	11.9	550	10	US-09-976-740-47

16	115	11.9	550	12	US-10-616-187-47	Sequence 47, Appl
17	115	11.9	550	14	US-10-023-529-47	Sequence 47, Appl
18	115	11.9	550	14	US-10-023-523-47	Sequence 47, Appl
19	113.5	11.7	336	12	US-10-264-049-2878	Sequence 2878, Ap
20	112.5	11.6	635	10	US-09-738-626-6614	Sequence 6614, Ap
21	110	11.4	418	9	US-09-795-668-3	Sequence 3, Appl
22	110	11.4	418	9	US-09-795-666-3	Sequence 3, Appl
23	110	11.4	418	10	US-09-946-807-3	Sequence 3, Appl
24	110	11.4	1023	11	US-09-893-519A-14	Sequence 14, Appl
25	108	11.2	682	15	US-10-156-761-12088	Sequence 12088, A
26	107.5	11.1	298	15	US-10-156-761-9483	Sequence 9483, Ap
27	107	11.1	674	15	US-10-156-761-9618	Sequence 9618, Ap
28	106.5	11.0	505	12	US-10-168-097A-56	Sequence 56, Appl
29	106.5	11.0	505	12	US-10-239-431A-36	Sequence 36, Appl
30	106	11.0	960	12	US-10-342-331-5	Sequence 5, Appl
31	105	10.9	2116	12	US-10-224-999A-3475	Sequence 3475, Ap
32	104	10.8	250	12	US-10-262-439-31	Sequence 31, Appl
33	104	10.8	250	15	US-10-218-654-31	Sequence 31, Appl
34	104	10.8	268	12	US-10-262-439-23	Sequence 23, Appl
35	104	10.8	268	15	US-10-218-654-23	Sequence 23, Appl
36	104	10.8	276	12	US-10-262-439-26	Sequence 26, Appl
37	104	10.8	276	12	US-10-218-654-26	Sequence 26, Appl
38	104	10.8	294	12	US-10-262-439-7	Sequence 7, Appl
39	104	10.8	294	15	US-10-218-654-7	Sequence 7, Appl
40	104	10.8	859	15	US-10-156-761-8128	Sequence 8128, Ap
41	103.5	10.7	531	10	US-09-925-300-1444	Sequence 1444, Ap
42	103.5	10.7	638	15	US-10-038-010-4	Sequence 4, Appl
43	103	10.7	710	12	US-10-104-047-3402	Sequence 3402, Ap
44	103	10.7	1003	12	US-10-094-749-2528	Sequence 2528, Ap
45	102.5	10.6	19662	12	US-10-084-846A-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-10-008-063-2
; Sequence 2, Application US/10008063
; Publication No. US20030092164A1
; GENERAL INFORMATION:
; APPLICANT: Gross, Jane A.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Henne, Randal M.
; APPLICANT: Grant, Francis, J.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor
; FILE REFERENCE: 00-103
; CURRENT APPLICATION NUMBER: US/10/008.063
; CURRENT FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-008-063-2

Query Match	98.8%	Score	954.5	DB	15	Length	184
Best Local Similarity	99.5%	Pred. No.	8.2e-69				
Matches	184	Conservative	0	Mismatches	0	Indels	1
Gaps	1						
QY	1	MRRGRSLRGDAPPTFCVPAECFDLLVRHCVACGLLRTPRPKPKXAGASSPAPRTALQP	60				
Db	1	MRRGRSLRGDAPPTFCVPAECFDLLVRHCVACGLLRTPRPKP-AGASSPAPRTALQP	59				
QY	61	QSVGAGAGEAALPLGLLFGAPALLGLALVLVLVGLVSWRRORRLGASAPDG	120				
Db	60	QSVGAGAGEAALPLGLLFGAPALLGLALVLVLVGLVSWRRORRLGASAPDG	119				
QY	121	DKDAPELDKVIILSPGISDATAPAPPPGDDPTTTPPGHSPVPATLSTELVTTKTA	180				
Db	120	DKDAPELDKVIILSPGISDATAPAPPPGDDPTTTPPGHSPVPATLSTELVTTKTA	179				
QY	181	GPEQ	185				

```
Db      180 GPEQ 184
|||||
RESULT 2
US-10-152-363A-60
; Sequence 60, Application US/10152363A
; Publication No. US20030103986A1
; GENERAL INFORMATION:
; APPLICANT: Rixon, Mark W.
; APPLICANT: Gross, Jane A.
; TITLE OF INVENTION: TAC1-Immunoglobulin Fusion Proteins
; FILE REFERENCE: 01-20
; CURRENT APPLICATION NUMBER: US/10/152,363A
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 60/293,343
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 60
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-152-363A-60

Query Match      98.8%; Score 954.5; DB 15; Length 184;
Best Local Similarity 99.5%; Pred. No. 8.2e-69;
Matches 184; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MRGRSLRGDAPATPCVPACFDLLVHCVACGLLRTPRPKXAGASSAPRTALQP 60
Db 1 MRGRSLRGDAPATPCVPACFDLLVHCVACGLLRTPRPKP-AGASSAPRTALQP 59
QY 61 QESVAGAGAAALPLGLLFGAPALLGLVLAIVLVGLVSWRRQRRLRGASSAEAPDG 120
Db 60 QESVAGAGAAALPLGLLFGAPALLGLVLAIVLVGLVSWRRQRRLRGASSAEAPDG 119
QY 121 DKDAPEPLDKVIIISPGISDATAPAWPPGDDGTTTPPGHSHVVPVPA TELGSELVTTKTA 180
Db 120 DKDAPEPLDKVIIISPGISDATAPAWPPGDDGTTTPPGHSHVVPVPA TELGSELVTTKTA 179
QY 181 GPEQ 185
|||||
Db 180 GPEQ 184

RESULT 3
US-10-251-947-2
; Sequence 2, Application US/10251947
; Publication No. US2003009990A1
; GENERAL INFORMATION:
; APPLICANT: Hsu, Hailing
; TITLE OF INVENTION: TALL-1 Receptor Molecules and Uses Thereof
; FILE REFERENCE: 01-1160-A
; CURRENT APPLICATION NUMBER: US/10/251,947
; CURRENT FILING DATE: 2002-09-20
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-251-947-2

Query Match      85.5%; Score 825.5; DB 15; Length 185;
Best Local Similarity 85.9%; Pred. No. 1.7e-56;
Matches 159; Conservative 7; Mismatches 18; Indels 1; Gaps 1;

QY 1 MRGRSLRGDAPATPCVPACFDLLVHCVACGLLRTPRPKXAGASSAPRTALQP 60
Db 1 MRGRSLRGDAPATPCVPACFDLLVHCVACGLLRTPRPKP-AGASSAPRTALQP 60
QY 61 QESVAGAGAAALPLGLLFGAPALLGLVLAIVLVGLVSWRRQRRLRGASSAEAPDG 120

Db      180 GPEQ 184
|||||
RESULT 4
US-10-251-947-4
; Sequence 4, Application US/10251947
; Publication No. US2003009990A1
; GENERAL INFORMATION:
; APPLICANT: Hsu, Hailing
; TITLE OF INVENTION: TALL-1 Receptor Molecules and Uses Thereof
; FILE REFERENCE: 01-1160-A
; CURRENT APPLICATION NUMBER: US/10/251,947
; CURRENT FILING DATE: 2002-09-20
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-251-947-4

Query Match      78.2%; Score 755.5; DB 15; Length 171;
Best Local Similarity 79.3%; Pred. No. 6e-53;
Matches 146; Conservative 7; Mismatches 18; Indels 13; Gaps 1;

QY 1 MRGRSLRGDAPATPCVPACFDLLVHCVACGLLRTPRPKXAGASSAPRTALQP 60
Db 1 MRGRSLRGDAPATPCVPACFDLLVHCVACGLLRTPRPKP-AGASSAPRTALQP 60
QY 61 QESVAGAGAAALPLGLLFGAPALLGLVLAIVLVGLVSWRRQRRLRGASSAEAPDG 120
Db 61 QESVGTGSGEVSLLPLGLLFGAPALLGLVLAIVLVGLVSWRRQRRLRGASSAEAPDG 120
QY 121 DKDAPEPLDKVIIISPGISDATAPAWPPGDDGTTTPPGHSHVVPVPA TELGSELVTTKTA 180
Db 121 DK-AGTDTAPAWPPGDDGTTTPPGHSHVVPVPA TELGSELVTTKTA 167
QY 181 GPEQ 184
|||||
Db 168 GPEQ 171

RESULT 5
US-10-251-947-7
; Sequence 7, Application US/10251947
; Publication No. US2003009990A1
; GENERAL INFORMATION:
; APPLICANT: Hsu, Hailing
; TITLE OF INVENTION: TALL-1 Receptor Molecules and Uses Thereof
; FILE REFERENCE: 01-1160-A
; CURRENT APPLICATION NUMBER: US/10/251,947
; CURRENT FILING DATE: 2002-09-20
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-251-947-7

Query Match      78.2%; Score 755.5; DB 15; Length 171;
Best Local Similarity 79.3%; Pred. No. 6e-53;
Matches 146; Conservative 7; Mismatches 18; Indels 13; Gaps 1;
```


NAME/KEY: UNSURE
LOCATION: (137)
OTHER INFORMATION: "Xaa" can be any naturally occurring amino acid,
FEATURE:
NAME/KEY: UNSURE
LOCATION: (138)
OTHER INFORMATION: "Xaa" can be any naturally occurring amino acid,
OTHER INFORMATION: or is absent.
US-10-251-947-14

Query Match 77.2%; Score 746; DB 15; Length 186;
Best Local Similarity 79.0%; Pred. No. 3.8e-52; Indels 2; Gaps 1;
Matches 147; Conservative 7; Mismatches 30;
QY 1 MRGPRSLRGDAPATPCVPAECFDLLVRHCVACGLLTPRPKPKXAGASSPAPRTALQP 60
DB 1 MRGPRSLRGDAPATPCVPAECFDLLVRHCVACGLLTPRPKPKXAGASSPAPRTALQP 60
QY 61 QESVCGAGAGEAALPLGILLFCAPALLGLALVLAIVGLVSWRRORRLRGASSAEAPDG 120
DB 61 QESVGTSGEVSLEPLGILLFCAPALLGLVLAIVGLVSWRRORRLRGASSAEAPDG 120
QY 121 DK--DAPEPLDKVILSPGISDATAPAWPPPGEDPGTTPPGHSVVPVPA TELGSTELVTTK 178
DB 121 DKAXXXXXXXXXXXXXXGTTDATAPAWPPPGEDQGTTPPGHSIPVPA TELGSTELVTTK 180
QY 179 TAGPEQ 184
DB 181 TAGPEQ 186

RESULT 8
US-10-008-063-13
Sequence 13, Application US/10008063
Publication No. US20030092164A1
GENERAL INFORMATION:
APPLICANT: Gross, Jane A.
APPLICANT: Xu, Wenfeng
APPLICANT: Henne, Randal M.
APPLICANT: Grant, Francis, J.
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor
FILE REFERENCE: 00-103
CURRENT APPLICATION NUMBER: US/10/008,063
CURRENT FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13
LENGTH: 175
TYPE: PRT
ORGANISM: Mouse
US-10-008-063-13

Query Match 42.5%; Score 411; DB 15; Length 175;
Best Local Similarity 55.8%; Pred. No. 2e-25; Indels 16; Gaps 6;
Matches 101; Conservative 9; Mismatches 55;
QY 6 RSLRGDAPATPCVPAECFDLLVRHCVACGLLTPRPKPKXAGASSPAPRTALQPOESVG 65
DB 9 RSRSRDSVPTQCNQTECFDPLVRNCVSCLEFHTP---DTGHTSLEFPGTALQPOE--- 62
QY 66 AGAGAAALPLGILLFCAPALLGLALVLAIVGLVSWRRORRLRGASSAEAPDGDKDA 124
DB 63 ---GSALPVDVALLVGAALLGLLALVLAIVGLVSWRRORRLRGASSAEAPDGDKDA 114
QY 125 -PEPLDKVILSPGISDATAPAWPPPGEDPGTTPPGHSVVPVPA TELGSTELVTTKTAGE 183
DB 115 QOESLENVFPSSPTPHASAPTWPPLKEDADALSALPHRSVFPVPA TELGSTELVTTKTAGE 174
QY 184 Q 184
DB 175 Q 175

RESULT 9
US-10-008-063-42
Sequence 42, Application US/10008063
Publication No. US20030092164A1
GENERAL INFORMATION:
APPLICANT: Gross, Jane A.
APPLICANT: Xu, Wenfeng
APPLICANT: Henne, Randal M.
APPLICANT: Grant, Francis, J.
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor
FILE REFERENCE: 00-103
CURRENT APPLICATION NUMBER: US/10/008,063
CURRENT FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 42
LENGTH: 328
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Ztnfr12-tcs-FC5.
US-10-008-063-42

Query Match 38.7%; Score 373.5; DB 15; Length 328;
Best Local Similarity 98.6%; Pred. No. 3.9e-22; Indels 1; Gaps 1;
Matches 72; Conservative 0; Mismatches 0;
QY 1 MRGPRSLRGDAPATPCVPAECFDLLVRHCVACGLLTPRPKPKXAGASSPAPRTALQP 60
DB 20 MRGPRSLRGDAPATPCVPAECFDLLVRHCVACGLLTPRPKPKXAGASSPAPRTALQP 78
QY 61 QESVCGAGAGEAAL 73
DB 79 QESVCGAGAGEAAL 91

RESULT 10
US-10-145-206-195
Sequence 195, Application US/10145206
Publication No. US20030195156A1
GENERAL INFORMATION:
APPLICANT: MIN, HOSUNG
APPLICANT: HSU, HAILING
APPLICANT: ZHONG, FEI
TITLE OF INVENTION: PEPTIDES AND RELATED MOLECULES THAT BIND TO TALL-1
FILE REFERENCE: A-743
CURRENT APPLICATION NUMBER: US/10/145,206
CURRENT FILING DATE: 2002-05-13
PRIOR APPLICATION NUMBER: US 60/290,196
PRIOR FILING DATE: 2001-05-11
NUMBER OF SEQ ID NOS: 197
SOFTWARE: Patent in version 3.1
SEQ ID NO 195
LENGTH: 38
TYPE: PRT
ORGANISM: Human
US-10-145-206-195

Query Match 18.4%; Score 178; DB 12; Length 38;
Best Local Similarity 84.2%; Pred. No. 1.6e-07; Indels 0; Gaps 0;
Matches 32; Conservative 1; Mismatches 5;
QY 1 MRGPRSLRGDAPATPCVPAECFDLLVRHCVACGLL 38
DB 1 MRGPRSLRGDAPATPCVPAECFDLLVRHCVACGLL 38
RESULT 11
US-10-271-343-32
Sequence 32, Application US/10271343
Publication No. US20030166003A1
GENERAL INFORMATION:

APPLICANT: Cochran, Andrea G.
APPLICANT: Skelton, Nicholas J.
APPLICANT: Starovasinik, Melissa A.
TITLE OF INVENTION: A STRUCTURED PEPTIDE SCAFFOLD FOR DISPLAYING TURN LIBRARIES
TITLE OF INVENTION: ON PHAGE
FILE REFERENCE: 11669.116US11
CURRENT APPLICATION NUMBER: US/10/271,343
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: US 09/592,695
PRIOR FILING DATE: 2000-06-13
PRIOR APPLICATION NUMBER: US 60/139,017
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patent in version 3.1
SEQ ID NO 32
LENGTH: 26
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Peptide
US-10-271-343-32

Query Match 15.4%; Score 149; DB 12; Length 26;
Best Local Similarity 100.0%; Pred. No. 2.2e-05;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 TPCVPAECFDLLVHVCACGLLTPT 42
DB 1 TPCVPAECFDLLVHVCACGLLTPT 26

RESULT 12
US-10-084-846A-7
Sequence 7, Application US/10084846A
Publication No. US20040006026A1
GENERAL INFORMATION:
APPLICANT: WEITNAUER, GABRIELE
APPLICANT: MUHLENWEG, AGNES
APPLICANT: TREFFER, AXEL
APPLICANT: BECHTHOLD, ANDREAS
TITLE OF INVENTION: AVILAMYCIN DERIVATIVES
FILE REFERENCE: 1974-005
CURRENT APPLICATION NUMBER: US/10/084,846A
CURRENT FILING DATE: 2003-02-25
PRIOR APPLICATION NUMBER: PCT/EP01/09815
PRIOR FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: DE 101 09 166.4
PRIOR FILING DATE: 2001-02-25
NUMBER OF SEQ ID NOS: 120
SOFTWARE: Patent in Ver. 3.2
SEQ ID NO 7
LENGTH: 19652
TYPE: PRT
ORGANISM: Streptomyces viridochromogenes
FEATURE:
OTHER INFORMATION: Protein 2: amino acid sequence encoded by coding strand 2.
OTHER INFORMATION: Start codon: gat, Start position: nucleotide 2.
US-10-084-846A-7

Query Match 12.5%; Score 121; DB 12; Length 19652;
Best Local Similarity 30.5%; Pred. No. 4.7;
Matches 61; Conservative 8; Mismatches 65; Indels 66; Gaps 13;

QY 2 RRG--PRSLGRD--APAPTFCVPAECFDLLVHVCACGLLTPTPKXAG-ASSPAPRT 56
DB 2312 RRGPRFARSVRGSPRPAPVVRPAP-----RTACAAGLPPAP-PRPAAGRASASSAPRP 2364

QY 57 ALQPOESVGACGAEALPLGLFGAPALLGLALVLVLGVSN-----RRQRRL 109
DB 2365 PRRP-----GVPRGP-----PPPARARP-----VRSGARCPRCVRC 2401

QY 110 -----RGASSAEAPDGDKDAPEFLDKVII-----LSPGISDATAPAWPPG-----EDFGT 155

Db 2402 CFVQPRRSAGRRPPSGRSAAARPRGAGAGTSRRARFGRPSGTSPSPPPPGAACPRGFTA 2461

QY 156 TTPG-----HSVPVP 165
DB 2462 GPPGPARAGPVAHGVSVP 2481

RESULT 13
US-08-736-019-170
Sequence 170, Application US/08736019
Publication No. US20030207799A1
GENERAL INFORMATION:
APPLICANT: Goodearl, Andrew
APPLICANT: Stroobant, Paul
APPLICANT: Minghetti, Luisa
APPLICANT: Waterfield, Michael
APPLICANT: Marchionni, Mark
APPLICANT: Chen, Mario
APPLICANT: Hiles, Ian
TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
TITLE OF INVENTION: PREPARATION AND USE
NUMBER OF SEQUENCES: 189
CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible Pentium
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/736,019
FILING DATE: 22-OCT-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/471,833
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/036,555
FILING DATE: 24-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/965,173
FILING DATE: 23-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/907,138
FILING DATE: 30-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/940,389
FILING DATE: 03-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/863,703
FILING DATE: 03-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UK 91 07566.3
FILING DATE: 10-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Slicker-Brady, Kristina
REGISTRATION NUMBER: 39,109
REFERENCE/DOCKET NUMBER: 04585/00200Q
TELEPHONE: (617) 428-0200
TELEFAX: (617) 428-7045
TELEX:
INFORMATION FOR SEQ ID NO: 170:
SEQUENCE CHARACTERISTICS:
LENGTH: 422
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear

US-08-736-019-170

Query Match 12.2%; Score 118; DB 7; Length 422;
 Best Local Similarity 28.3%; Pred. No. 0.13; 51; Indels 70; Gaps 11;
 Matches 54; Conservative 16; Mismatches 15; Indels 88; Gaps 11;
 QY 2 RRGSRSLRGDAPAPPTPCVPAECFDLLVRHCVACGLLRTTPRKPXAGASSAP-----54
 Db 4 RRAPRR-SGRPGF-----RAQRPGSAARSSPPLPLLL 38
 QY 55 --RTALQPOESVAGAGEAALPL-PGLLFGAALLG-----LALVIALVLGLVSWRROR 107
 Db 39 LGTAALAP-----GAAGNEAAPAGASVCYSSPSSVQELAQRAAVIEKVHPQRQQ 94
 QY 108 -----RLRGASSAEP--DGDKDAPELDKVIILSPGISDATAP-AMPPPGSDP-----GT 155
 Db 95 GALDRKAAAGAGAGAWGSDREPP-----AAGPRALGPAPAEPLLAANGT 139
 QY 156 TPGHSPVPEA 166
 Db 140 VFSWPTAPVPS 150

RESULT 14

US-10-177-293-214
 ; Sequence 214, Application US/10177293
 ; Publication No. US20030124128A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lillie, James
 ; APPLICANT: Glatt, Karen
 ; APPLICANT: Zhao, Xumei
 ; APPLICANT: Ganavarpu, Manjula
 ; APPLICANT: Kamatkar, Shubhangi
 ; APPLICANT: Mertens, Maureen
 ; APPLICANT: Myer, Vic
 ; APPLICANT: Wang, Youzhen
 ; APPLICANT: Xu, Yongyao
 ; APPLICANT: Hoersch, Sebastian
 ; APPLICANT: Monahan, John
 ; APPLICANT: Meyers, Rachel E.
 ; APPLICANT: Bast Jr., Robert C.
 ; APPLICANT: Hortobagyi, Gabriel N.
 ; APPLICANT: Fuzetel, Lajos
 ; APPLICANT: Meric, Funda
 ; APPLICANT: Sahin, Aysegul
 ; APPLICANT: Mills, Gordon B.
 ; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
 ; FILE REFERENCE: MRI-038
 ; CURRENT APPLICATION NUMBER: US/10/177,293
 ; PRIOR FILING DATE: 2002-06-21
 ; PRIOR APPLICATION NUMBER: US 60/299,887
 ; PRIOR FILING DATE: 2001-06-21
 ; PRIOR APPLICATION NUMBER: US 60/301,572
 ; PRIOR FILING DATE: 2001-06-27
 ; PRIOR APPLICATION NUMBER: US 60/306,501
 ; PRIOR FILING DATE: 2001-07-18
 ; PRIOR APPLICATION NUMBER: US 60/325,002
 ; PRIOR FILING DATE: 2001-09-25
 ; PRIOR APPLICATION NUMBER: US 60/362,585
 ; PRIOR FILING DATE: 2002-03-05
 ; PRIOR APPLICATION NUMBER: US 60/xxx,xxx
 ; PRIOR FILING DATE: 2002-05-14
 ; NUMBER OF SEQ ID NOS: 506
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 214
 ; LENGTH: 356
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-177-293-214

Query Match 11.9%; Score 115; DB 15; Length 356;
 Best Local Similarity 24.7%; Pred. No. 0.19;

Matches 56; Conservative 15; Mismatches 68; Indels 88; Gaps 11;
 QY 5 PPS-LRGRDAPA-----PTPCVPAECFDLLVRHCVACGLLRTTPR-----KPXA 47
 Db 66 PPSQKRAEDGALPPPPPLPA-----APPAPFPWMKEKSAKPSQ 109
 QY 48 GASSPAPTALQPOESVAGAGEAALPLPG-----LL-----FG 81
 Db 110 SATSPSPAASAVPASGVSPADGLGLPEAGGGGARLRTAYTNTQILLEKEHFHNKYL 169
 QY 82 APALLGLALVIALVLGLVSW--RRORRLRGASSAEPDGDKDAPELDKVI-----I 133
 Db 170 RPRVEIALDLITERQVKNWFQNRMKHKQTOHREPPDGEPAFCGALIEDICDPAEPA 229
 QY 134 LSPGISDATAPAW-----PP-----EDPGTTPPG 159
 Db 230 ASFGGPSASRAAWEACCHPEVVFPGALSADPRPLAVRLEGAGASSPG 276

RESULT 15

US-09-976-740-47
 ; Sequence 47, Application US/09976740
 ; Publication No. US20020194633A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lees, Ann M.
 ; APPLICANT: Lees, Robert S.
 ; APPLICANT: Law, Simon W.
 ; APPLICANT: Arjona, Anibal A.
 ; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
 ; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
 ; FILE REFERENCE: 10797-004001
 ; CURRENT APPLICATION NUMBER: US/09/976,740
 ; PRIOR FILING DATE: 2001-10-12
 ; PRIOR APPLICATION NUMBER: 09/616,289
 ; PRIOR FILING DATE: 2000-07-14
 ; PRIOR APPLICATION NUMBER: US 08/979,608
 ; PRIOR FILING DATE: 1997-11-26
 ; PRIOR APPLICATION NUMBER: US 60/031,930
 ; PRIOR FILING DATE: 1996-11-27
 ; PRIOR APPLICATION NUMBER: US 60/048,547
 ; PRIOR FILING DATE: 1997-06-03
 ; NUMBER OF SEQ ID NOS: 53
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 47
 ; LENGTH: 550
 ; TYPE: PRT
 ; ORGANISM: Oryctolagus cuniculus
 US-09-976-740-47

Query Match 11.9%; Score 115; DB 10; Length 550;
 Best Local Similarity 26.7%; Pred. No. 0.31;
 Matches 54; Conservative 10; Mismatches 66; Indels 72; Gaps 9;
 QY 2 RRG-----PRSLRG-----RDAPAPTPCVPAECFDLLVRHCVACGLLRTTPRKPXAGASS 51
 Db 104 RRGATPPAPRPRGPGPAAAAAPPPTAPP-----PPAPFAAAAA 144
 QY 52 P--APTALQPOESVAGAGEAALPLGGLFCAPALLGLALVIALVLGLVSWRRORRL 109
 Db 145 PARAPRAA-----AAAAAATAPSPG-----PAQPG-----PRAQRAA 177
 QY 110 RGAS-----SAEAPDGDKDAPELDKVIILSPGISDATAPAWPPPGDPTTPPGH 160
 Db 178 PLAAPPAPAAAPPAGPRAPPAANAARSPPLPPPPPPAPPPQOQQPPPPPP 237
 QY 161 SVPVPATELGSTELVTTKAGP 182
 Db 238 QQPOPPPEGGA-----ARAGGP 254

Search completed: February 5, 2004, 18:09:53
 Job time : 31.8333 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 5, 2004, 17:57:39 ; Search time 14.9028 Seconds
(without alignments)
525.238 Million cell updates/sec

Title: US-10-045-574B-27
Perfect score: 966
Sequence: 1 MRGRPSLRGRDAPAPTCV.....ATELGSTELVTTKTAGEPQQ 185

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /cgn2.6/prodata/1/1aa/5A_COMB.pep:*
2: /cgn2.6/prodata/1/1aa/5B_COMB.pep:*
3: /cgn2.6/prodata/1/1aa/6A_COMB.pep:*
4: /cgn2.6/prodata/1/1aa/6B_COMB.pep:*
5: /cgn2.6/prodata/1/1aa/PCTUS_COMB.pep:*
6: /cgn2.6/prodata/1/1aa/backfiles.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	118	12.2	248	3	US-08-341-018-52
2	118	12.2	248	3	US-08-470-335-210
3	118	12.2	248	3	US-08-470-333-210
4	118	12.2	248	4	US-08-467-602-207
5	118	12.2	248	4	US-08-467-602-404
6	118	12.2	349	3	US-08-470-335-188
7	118	12.2	382	4	US-08-467-602-382
8	118	12.2	405	4	US-08-467-602-384
9	118	12.2	411	3	US-08-470-339-189
10	118	12.2	414	3	US-08-470-339-188
11	118	12.2	422	1	US-08-036-5558-170
12	118	12.2	422	1	US-08-469-569-170
13	118	12.2	422	1	US-08-428-926-3
14	118	12.2	422	1	US-08-249-322A-170
15	118	12.2	422	1	US-08-428-927-3
16	118	12.2	422	1	US-08-428-298-3
17	118	12.2	422	1	US-08-339-517-3
18	118	12.2	422	1	US-08-469-528A-170
19	118	12.2	422	2	US-08-734-591A-170
20	118	12.2	422	2	US-08-469-560-170
21	118	12.2	422	3	US-08-341-018-72
22	118	12.2	422	3	US-08-470-335-170
23	118	12.2	422	3	US-08-735-021-170
24	118	12.2	422	3	US-08-734-664A-170
25	118	12.2	422	3	US-08-339-170
26	118	12.2	422	4	US-08-467-602-170
27	118	12.2	422	4	US-08-467-602-324

28	118	12.2	422	5	PCT-US94-05083C-166	Sequence 166, App
29	118	12.2	422	5	PCT-US94-05083C-185	Sequence 185, App
30	118	12.2	422	5	PCT-US95-06846A-170	Sequence 170, App
31	118	12.2	425	3	US-08-470-335-226	Sequence 226, App
32	118	12.2	425	4	US-08-457-602-320	Sequence 320, App
33	118	12.2	445	4	US-08-457-602-328	Sequence 328, App
34	118	12.2	456	3	US-08-470-335-246	Sequence 246, App
35	118	12.2	456	4	US-08-467-602-303	Sequence 303, App
36	118	12.2	456	4	US-08-467-602-366	Sequence 366, App
37	118	12.2	459	3	US-08-470-335-239	Sequence 239, App
38	118	12.2	459	4	US-08-467-602-299	Sequence 299, App
39	118	12.2	459	4	US-08-467-602-362	Sequence 362, App
40	118	12.2	479	4	US-08-457-602-307	Sequence 307, App
41	118	12.2	479	4	US-08-467-602-370	Sequence 370, App
42	118	12.2	490	4	US-08-467-602-345	Sequence 345, App
43	118	12.2	493	4	US-08-467-602-341	Sequence 341, App
44	118	12.2	513	4	US-08-467-602-349	Sequence 349, App
45	118	12.2	601	3	US-08-470-335-233	Sequence 233, App

ALIGNMENTS

RESULT 1
US-08-341-018-52
; Sequence 52, Application US/08341018A
; Patent No. 6087323
; GENERAL INFORMATION:
; APPLICANT: Gwynne, David I.
; APPLICANT: Mahanthappa, Nagesh K.
; APPLICANT: Marchionni, Mark A.
; APPLICANT: Bermingham-McDonogh, Olivia
; APPLICANT: Goldin, Stanley M.
; APPLICANT: McBurney, Robert N.
; TITLE OF INVENTION: USE OF NEUREGULINS AS MODULATORS OF
; FILE OF INVENTION: CELLULAR COMMUNICATION
; FILE REFERENCE: 04585/041001
; CURRENT APPLICATION NUMBER: US/08/341.018A
; CURRENT FILING DATE: 1994-11-17
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-341-018-52

Query Match	12.2%	Score 118;	DB 3;	Length 248;
Best Local Similarity	28.3%	Pred. No. 0.0024;		
Matches	54;	Conservative 16;	Mismatches 51;	Indels 70; Gaps 11;
QY	2	RRGRPSLRGRDAPAPTCVPAECFDLLVRHCVCAGLLRTPRPKFXAGASSAP	-----	54
Db	4	RRAPRR-SGRPOP	-----	RAQRPGSAARSPPLPILLLL 38
QY	55	--RTALQVESVGAGGAAALPL-PGLLFGAPALLG---	LALVLALVGLYSWREROR	107
Db	39	LGTAALAP----	GAAGNEAAPAGASCYSPSPSVQVOLAQRAAVVIEGKHVPQRQQ	94
QY	108	----RLRGASSAEAP--DGDKDAPEPLDKVILSPGISDATAP--AWPPPGEDP	-----	GT 155
Db	95	GALDRKAAAGAGAGAWGSDREPP-----	-----	AAGPRALGPAAEPEPLAANGT 139
QY	156	TPPGHSPVPA 166		
Db	140	VPSWPTAPVPS 150		
RESULT 2				
US-08-470-335-210				
; Sequence 210, Application US/08470335F				
; Patent No. 6147190				
; GENERAL INFORMATION:				

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; APPLICANT: GOODEARL, ANDREW
; APPLICANT: STROOBANT, PAUL
; APPLICANT: MINGHETTI, LUISA
; APPLICANT: WATERFIELD, MICHAEL
; APPLICANT: MARCHIONNI, MARK
; APPLICANT: CHEN, MARIO S.
; APPLICANT: HILES, IAN
; TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
; PREPARATION AND USE
; FILE REFERENCE: 04585/002008
; CURRENT APPLICATION NUMBER: US/08/470,339F
; EARLIER APPLICATION NUMBER: 08/036,555
; EARLIER FILING DATE: 1993-03-24
; NUMBER OF SEQ ID NOS: 252
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 210
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-470-339-210

Query Match 12.2%; Score 118; DB 3; Length 248;
Best Local Similarity 28.3%; Pred. No. 0.0024;
Matches 54; Conservative 16; Mismatches 51; Indels 70; Gaps 11;

QY 2 RRGPSRLGRDAPAPTCCVPACFDLLVRHCVACGLLRTPRPKPXAGASSPAP----- 54
DB 4 RRAPRR-SGRPGP-----RAQPGSAARSSPPLPLPLLLL 38
QY 55 --RTALQPOESVGAGAGEAALPL-PGLLFGAPALLG----LALVLALVLVLVSWRRQR 107
DB 39 LGTAALAP---GAAAGNEAAPAGASVCYSSPPSVGSVQELAQRAAVVIEGKVHPQRQQ 94
QY 108 ----RLRGASSAEAP--DGDKDAPEPLDKVILSPGISDATAP-AWPPPGEDP-----GT 155
DB 95 GALDRKAAAAGAGAGANGDREPP-----AAGPRALGPPAEPLLAANGT 139
QY 156 TPGHSHVVPVA 166
DB 140 VPSWPTAPVPS 150

RESULT 4
US-08-467-602-207
; Sequence 207, Application US/08467602C
; Patent No. 6444642
; GENERAL INFORMATION:
; APPLICANT: Sklar, Robert
; APPLICANT: Marchionni, Mark
; APPLICANT: Gwynne, David I.
; TITLE OF INVENTION: METHODS FOR TREATING MUSCLE DISEASES AND
; FILE REFERENCE: 04585/028003
; CURRENT APPLICATION NUMBER: US/08/467,602C
; CURRENT FILING DATE: 1995-06-06
; EARLIER APPLICATION NUMBER: 08/209,204
; EARLIER FILING DATE: 1994-03-08
; EARLIER APPLICATION NUMBER: 08/059,022
; EARLIER FILING DATE: 1993-05-06
; NUMBER OF SEQ ID NOS: 420
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 207
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-467-602-207

Query Match 12.2%; Score 118; DB 4; Length 248;
Best Local Similarity 28.3%; Pred. No. 0.0024;
Matches 54; Conservative 16; Mismatches 51; Indels 70; Gaps 11;

QY 2 RRGPSRLGRDAPAPTCCVPACFDLLVRHCVACGLLRTPRPKPXAGASSPAP----- 54
DB 4 RRAPRR-SGRPGP-----RAQPGSAARSSPPLPLPLLLL 38
QY 55 --RTALQPOESVGAGAGEAALPL-PGLLFGAPALLG----LALVLALVLVLVSWRRQR 107
DB 39 LGTAALAP---GAAAGNEAAPAGASVCYSSPPSVGSVQELAQRAAVVIEGKVHPQRQQ 94
QY 108 ----RLRGASSAEAP--DGDKDAPEPLDKVILSPGISDATAP-AWPPPGEDP-----GT 155
DB 95 GALDRKAAAAGAGAGANGDREPP-----AAGPRALGPPAEPLLAANGT 139
QY 156 TPGHSHVVPVA 166
DB 140 VPSWPTAPVPS 150

RESULT 5
US-08-470-339-210
; Sequence 210, Application US/08470339C
; Patent No. 6232286
; GENERAL INFORMATION:
; APPLICANT: GOODEARL, ANDREW
; APPLICANT: STROOBANT, PAUL
; APPLICANT: MINGHETTI, LUISA
; APPLICANT: WATERFIELD, MICHAEL
; APPLICANT: MARCHIONNI, MARK
; APPLICANT: CHEN, MARIO S.
; APPLICANT: HILES, IAN
; TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
; PREPARATION AND USE
; FILE REFERENCE: 04585/002008
; CURRENT APPLICATION NUMBER: US/08/470,339C
; CURRENT FILING DATE: 1995-06-06
; EARLIER APPLICATION NUMBER: 08/036,555
; EARLIER FILING DATE: 1993-03-24
; EARLIER APPLICATION NUMBER: 07/940,389
; EARLIER FILING DATE: 1992-09-03
; EARLIER APPLICATION NUMBER: 07/907,138
; EARLIER FILING DATE: 1992-06-30
; EARLIER APPLICATION NUMBER: 07/863,703
; EARLIER FILING DATE: 1992-04-03
; EARLIER APPLICATION NUMBER: 91,07566.3 GB
; NUMBER OF SEQ ID NOS: 226
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 210
```

US-08-467-602-404

; Sequence 404, Application US/08467602C
; Patent No. 6444642

; GENERAL INFORMATION:

; APPLICANT: Sklar, Robert

; APPLICANT: Marchionni, Mark

; APPLICANT: Gwynne, David I.

; TITLE OF INVENTION: METHODS FOR TREATING MUSCLE DISEASES AND

; TITLE OF INVENTION: DISORDERS

; FILE REFERENCE: 04585/028003

; CURRENT APPLICATION NUMBER: US/08/467,602C

; CURRENT FILING DATE: 1995-06-06

; EARLIER APPLICATION NUMBER: 08/209,204

; EARLIER FILING DATE: 1994-03-08

; EARLIER APPLICATION NUMBER: 08/059,022

; EARLIER FILING DATE: 1993-05-06

; NUMBER OF SEQ ID NOS: 420

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 404

; LENGTH: 248

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-08-467-602-404

Query Match 12.2%; Score 118; DB 4; Length 248;

Best Local Similarity 28.3%; Pred. No. 0.0024;

Matches 54; Conservative 16; Mismatches 51; Indels 70; Gaps 11;

QY 2 RGRPSLRGRDAPPTPCVPAECFDLLVRHCVACGLLRTPRPKPXAGASSPAP-----54

DB 4 RRAPRR-SGRPGP-----RAQRPGSAAARSSPPLPLPLLLL 38

QY 55 --RTALQPOESVAGAGEAALPL-PGLFGAPALLG-----LALVLALVLVLGVSRRRQR 107

DB 39 LGTAALAP-----GAAAGNEAAPAGASVCYSSPPSVGSVOELAQRAAVVIEGKVPQRQQ 94

QY 108 ----RLRGASSAEAP--DGDKDAPEPLDKVILSPGISDATAP-AWPPPGEDP-----GT 155

DB 95 GALDRKAAAGAGAGAWGSDREPP-----AAGPRALGPPAEPEPLLAANGT 139

QY 156 TTPGHSHVPVPA 166

DB 140 VPSWPTAPVPS 150

RESULT 6

US-08-470-335-188

; Sequence 188, Application US/08470335F

; Patent No. 6147190

; GENERAL INFORMATION:

; APPLICANT: GOODEARL, ANDREW

; APPLICANT: STROOBANT, PAUL

; APPLICANT: MINGHETTI, LUISA

; APPLICANT: WATERFIELD, MICHAEL

; APPLICANT: MARCHIONNI, MARK

; APPLICANT: CHEN, MARIO S.

; APPLICANT: HILES, IAN

; TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR

; TITLE OF INVENTION: PREPARATION AND USE

; FILE REFERENCE: 04585/002008

; CURRENT APPLICATION NUMBER: US/08/470,335F

; CURRENT FILING DATE: 1995-06-06

; EARLIER APPLICATION NUMBER: 08/036,555

; EARLIER FILING DATE: 1993-03-24

; NUMBER OF SEQ ID NOS: 252

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 188

; LENGTH: 349

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-08-470-335-188

Query Match

12.2%; Score 118; DB 3; Length 349;

Best Local Similarity 28.3%; Pred. No. 0.0036;
Matches 54; Conservative 16; Mismatches 51; Indels 70; Gaps 11;

QY 2 RGRPSLRGRDAPPTPCVPAECFDLLVRHCVACGLLRTPRPKPXAGASSPAP-----54

DB 4 RRAPRR-SGRPGP-----RAQRPGSAAARSSPPLPLPLLLL 38

QY 55 --RTALQPOESVAGAGEAALPL-PGLFGAPALLG-----LALVLALVLVLGVSRRRQR 107

DB 39 LGTAALAP-----GAAAGNEAAPAGASVCYSSPPSVGSVOELAQRAAVVIEGKVPQRQQ 94

QY 108 ----RLRGASSAEAP--DGDKDAPEPLDKVILSPGISDATAP-AWPPPGEDP-----GT 155

DB 95 GALDRKAAAGAGAGAWGSDREPP-----AAGPRALGPPAEPEPLLAANGT 139

QY 156 TTPGHSHVPVPA 166

DB 140 VPSWPTAPVPS 150

RESULT 7

US-08-467-602-382

; Sequence 382, Application US/08467602C

; Patent No. 6444642

; GENERAL INFORMATION:

; APPLICANT: Sklar, Robert

; APPLICANT: Marchionni, Mark

; APPLICANT: Gwynne, David I.

; TITLE OF INVENTION: METHODS FOR TREATING MUSCLE DISEASES AND

; TITLE OF INVENTION: DISORDERS

; FILE REFERENCE: 04585/028003

; CURRENT APPLICATION NUMBER: US/08/467,602C

; CURRENT FILING DATE: 1995-06-06

; EARLIER APPLICATION NUMBER: 08/209,204

; EARLIER FILING DATE: 1994-03-08

; EARLIER APPLICATION NUMBER: 08/059,022

; EARLIER FILING DATE: 1993-05-06

; NUMBER OF SEQ ID NOS: 420

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 382

; LENGTH: 382

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: VARIANT

; LOCATION: (34)...(34)

; OTHER INFORMATION: Xaa is any amino acid

; US-08-467-602-382

Query Match 12.2%; Score 118; DB 4; Length 382;

Best Local Similarity 28.3%; Pred. No. 0.004;

Matches 54; Conservative 16; Mismatches 51; Indels 70; Gaps 11;

QY 2 RGRPSLRGRDAPPTPCVPAECFDLLVRHCVACGLLRTPRPKPXAGASSPAP-----54

DB 38 RRAPRR-SGRPGP-----RAQRPGSAAARSSPPLPLPLLLL 72

QY 55 --RTALQPOESVAGAGEAALPL-PGLFGAPALLG-----LALVLALVLVLGVSRRRQR 107

DB 73 LGTAALAP-----GAAAGNEAAPAGASVCYSSPPSVGSVOELAQRAAVVIEGKVPQRQQ 128

QY 108 ----RLRGASSAEAP--DGDKDAPEPLDKVILSPGISDATAP-AWPPPGEDP-----GT 155

DB 129 GALDRKAAAGAGAGAWGSDREPP-----AAGPRALGPPAEPEPLLAANGT 173

QY 156 TTPGHSHVPVPA 166

DB 174 VPSWPTAPVPS 184

RESULT 8

US-08-467-602-384

; Sequence 384, Application US/08467602C

Patent No. 6444642
; GENERAL INFORMATION:
; APPLICANT: Sklar, Robert
; APPLICANT: Marchionni, Mark
; APPLICANT: Gwynne, David I.
; TITLE OF INVENTION: METHODS FOR TREATING MUSCLE DISEASES AND
; FILE REFERENCE: 04585/028003
; CURRENT APPLICATION NUMBER: US/08/467,602C
; EARLIER FILING DATE: 1995-06-06
; EARLIER APPLICATION NUMBER: 08/209,204
; EARLIER FILING DATE: 1994-03-08
; EARLIER APPLICATION NUMBER: 08/059,022
; EARLIER FILING DATE: 1993-05-06
; NUMBER OF SEQ ID NOS: 420
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 384
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: VARIANT
; LOCATION: (34)...(34)
; OTHER INFORMATION: Xaa is any amino acid
US-08-467-602-384

Query Match 12.2%; Score 118; DB 4; Length 405;
Best Local Similarity 28.3%; Pred. No. 0.0043;
Matches 54; Conservative 16; Mismatches 51; Indels 70; Gaps 11;

QY 2 RRGPSRLGRDAPAPTFCVPAECFDLLVRHCACGLLRTPRPKFXAGASSPAP----- 54
DB 38 RRAPRR-SGRPGP-----RAQPGSAARSSPPLPLPLLLL 72
QY 55 --RTALQPQESVGAGAGEAALPL-PGLLFGAPALIG-----LALVLALVLVLVSWRRRQ 107
DB 73 LGTAALAP-----GAAAGNEAPAGASVCYSPSPSVQELAQRAAVVIEGKVHPQRQQ 128
QY 108 ---RLRGASSAEP--DGDKDAPPLDKVILSPGISDATAP-AWPPPGEDP-----GT 155
DB 129 GALDRKAAAGAGAGANGDREPP-----AAGPRALGPFAEPLLAANGT 173
QY 156 TPEGHSVPVPA 166
DB 174 VPSWPTADVPS 184

RESULT 9
US-08-470-339-189
; Sequence 189, Application US/08470339C
; Patent No. 6232286
; GENERAL INFORMATION:
; APPLICANT: GOODEARL, ANDREW
; APPLICANT: STROOBANT, PAUL
; APPLICANT: MINGHETTI, LUISA
; APPLICANT: WATERFIELD, MICHAEL
; APPLICANT: MARCHIONNI, MARK
; APPLICANT: CHEN, MARIO S.
; APPLICANT: HILES, IAN
; TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
; FILE REFERENCE: 04585/002008
; CURRENT APPLICATION NUMBER: US/08/470,339C
; CURRENT FILING DATE: 1995-06-06
; EARLIER FILING DATE: 1993-03-24
; EARLIER APPLICATION NUMBER: 08/036,555
; EARLIER FILING DATE: 1993-03-24
; EARLIER APPLICATION NUMBER: 07/940,389
; EARLIER FILING DATE: 1992-09-03
; EARLIER APPLICATION NUMBER: 07/907,138
; EARLIER FILING DATE: 1992-06-30
; EARLIER APPLICATION NUMBER: 07/863,703
; EARLIER FILING DATE: 1992-04-10
; EARLIER APPLICATION NUMBER: 91 07566.3 GB

; EARLIER FILING DATE: 1999-04-10
; NUMBER OF SEQ ID NOS: 226
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 189
; LENGTH: 411
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-470-339-189

Query Match 12.2%; Score 118; DB 3; Length 411;
Best Local Similarity 28.3%; Pred. No. 0.0044;
Matches 54; Conservative 16; Mismatches 51; Indels 70; Gaps 11;

QY 2 RRGPSRLGRDAPAPTFCVPAECFDLLVRHCACGLLRTPRPKFXAGASSPAP----- 54
DB 4 RRAPRR-SGRPGP-----RAQPGSAARSSPPLPLPLLLL 38
QY 55 --RTALQPQESVGAGAGEAALPL-PGLLFGAPALIG-----LALVLALVLVLVSWRRRQ 107
DB 39 LGTAALAP-----GAAAGNEAPAGASVCYSPSPSVQELAQRAAVVIEGKVHPQRQQ 94
QY 108 ---RLRGASSAEP--DGDKDAPPLDKVILSPGISDATAP-AWPPPGEDP-----GT 155
DB 95 GALDRKAAAGAGAGANGDREPP-----AAGPRALGPFAEPLLAANGT 139
QY 156 TPEGHSVPVPA 166
DB 140 VPSWPTADVPS 150

RESULT 10
US-08-470-339-189
; Sequence 188, Application US/08470339C
; Patent No. 6232286
; GENERAL INFORMATION:
; APPLICANT: GOODEARL, ANDREW
; APPLICANT: STROOBANT, PAUL
; APPLICANT: MINGHETTI, LUISA
; APPLICANT: WATERFIELD, MICHAEL
; APPLICANT: MARCHIONNI, MARK
; APPLICANT: CHEN, MARIO S.
; APPLICANT: HILES, IAN
; TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
; FILE REFERENCE: 04585/002008
; CURRENT APPLICATION NUMBER: US/08/470,339C
; CURRENT FILING DATE: 1995-06-06
; EARLIER FILING DATE: 1993-03-24
; EARLIER APPLICATION NUMBER: 08/036,555
; EARLIER FILING DATE: 1993-03-24
; EARLIER APPLICATION NUMBER: 07/940,389
; EARLIER FILING DATE: 1992-09-03
; EARLIER APPLICATION NUMBER: 07/907,138
; EARLIER FILING DATE: 1992-06-30
; EARLIER APPLICATION NUMBER: 07/863,703
; EARLIER FILING DATE: 1992-04-10
; EARLIER APPLICATION NUMBER: 91 07566.3 GB
; NUMBER OF SEQ ID NOS: 226
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 188
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-470-339-189

Query Match 12.2%; Score 118; DB 3; Length 414;
Best Local Similarity 28.3%; Pred. No. 0.0044;
Matches 54; Conservative 16; Mismatches 51; Indels 70; Gaps 11;

QY 2 RRGPSRLGRDAPAPTFCVPAECFDLLVRHCACGLLRTPRPKFXAGASSPAP----- 54
DB 4 RRAPRR-SGRPGP-----RAQPGSAARSSPPLPLPLLLL 38

QY 55 --RTALQFESVGAGAGAAALPL-PGLLFGAPALLG-----LALVLALVLGLVSWRRQR 107
Db 39 LGTAALAP-----GAAAGNEAAPAGASVCYSSPPSVGSVQELAQRAAVIEGKVHPQRRQ 94
QY 108 ----RLRGASSAEP--DGDKDAPPLDKVILSPGISDATAP--AWPPPGEDP-----GT 155
Db 95 GALDRKAAAGAGAGANGGDREPP-----AAGPRALGPAAEPLLAANGT 139
QY 156 TPGHSHVPVPA 166
Db 140 VPSWPTAPVPS 150

RESULT 11

US-08-036-555B-170
; Sequence 170, Application US/08036555B
; Patent No. 5530109
; GENERAL INFORMATION:
; APPLICANT: Goodearl, Andrew; Stroobant, Paul;
; APPLICANT: Minghetti, Luisa; Waterfield, Michael; Marchioni, Mark;
; APPLICANT: Chen, Maio Su; Hiles, Ian
; TITLE OF INVENTION: Glial Mitogenic Factors, Their
; TITLE OF INVENTION: Preparation and Use
; NUMBER OF SEQUENCES: 184
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/036,555B
; FILING DATE: 24-MAR-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/965,173
; FILING DATE: 23-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/940,389
; FILING DATE: 03-SEP-1992
; APPLICATION NUMBER: 07/907,138
; FILING DATE: 30-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/863,703
; FILING DATE: 03-APRIL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.K. 91 07566.3
; FILING DATE: 10-APRIL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Tsai, Christine H.
; REGISTRATION NUMBER: 34,266
; REFERENCE/DOCKET NUMBER: LUD 5250.4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 170:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 422
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-036-555B-170

Query Match 12.2%; Score 118; DB 1; Length 422;
Best Local Similarity 28.3%; Pred. No. 0.0045;
Matches 54; Conservative 16; Mismatches 51; Indels 70; Gaps 11;

QY 2 RRGPSRLGRDAPATPCVPAECFLLVHCVACGLLRTPRPKFXAGASSPAP----- 54
Db 4 RAAPRR-SGRPCP-----RAQPGSAARSSPPLPLPLLLL 38
QY 55 --RTALQFESVGAGAGAAALPL-PGLLFGAPALLG-----LALVLALVLGLVSWRRQR 107
Db 39 LGTAALAP-----GAAAGNEAAPAGASVCYSSPPSVGSVQELAQRAAVIEGKVHPQRRQ 94
QY 108 ----RLRGASSAEP--DGDKDAPPLDKVILSPGISDATAP--AWPPPGEDP-----GT 155
Db 95 GALDRKAAAGAGAGANGGDREPP-----AAGPRALGPAAEPLLAANGT 139
QY 156 TPGHSHVPVPA 166
Db 140 VPSWPTAPVPS 150

RESULT 12
US-08-469-569-170
; Sequence 170, Application US/08469569
; Patent No. 5606032
; GENERAL INFORMATION:
; APPLICANT: Goodearl, Andrew; Stroobant, Paul;
; APPLICANT: Minghetti, Luisa; Waterfield, Michael; Marchioni, Mark;
; APPLICANT: Chen, Maio Su; Hiles, Ian
; TITLE OF INVENTION: Glial Mitogenic Factors, Their
; TITLE OF INVENTION: Preparation and Use
; NUMBER OF SEQUENCES: 184
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,569
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/036,555
; FILING DATE: 24-MAR-1993
; APPLICATION NUMBER: 07/965,173
; FILING DATE: 23-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/940,389
; FILING DATE: 03-SEP-1992
; APPLICATION NUMBER: 07/907,138
; FILING DATE: 30-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/863,703
; FILING DATE: 03-APRIL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.K. 91 07566.3
; FILING DATE: 10-APRIL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Tsai, Christine H.
; REGISTRATION NUMBER: 34,266
; REFERENCE/DOCKET NUMBER: LUD 5250.4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 170:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 422
; TYPE: amino acid

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; STRANDEDNESS:
; TOPOLOGY: linear
US-08-429-926-3
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; Query Match 12.2%; Score 118; DB 1; Length 422;
; Best Local Similarity 28.3%; Pred. No. 0.0045;
; Matches 54; Conservative 16; Mismatches 51; Indels 70; Gaps 11;
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; QY 2 RRGPSLRGRDAPAPTCVPAECFDLLVRHCVACGLLRTPRKPXAGASSPAP-----54
; DB 4 RRAPRR-SGRPGP-----RAQPGSAARSPPLPLPLLLL 38
;
; QY 55 --RTALQPOESVAGAGERAALPL-PGLLFGAPALLG-----LALVLALVLVGLVSWRRRQR 107
; DB 39 LGTAALAP-----GAAAGNEAAPAGASVCYSSPPSVGSVOELAQRAAAVIEGKVHPQRQQ 94
;
; QY 108 ---RLRGASSAEAP--DGDKDAPEPLDKVILSPGISDATAP-AWPPPGEDP-----GT 155
; DB 95 GALDRKAAAAGAGAGANGGDREPP-----AAGPRALGPAPAEPLLAANGT 139
;
; QY 156 TPGCHSVVPVA 166
; DB 140 VPSWPTAPVPS 150
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; RESULT 14
; US-08-249-322A-170
; Sequence 170, Application US/08249322A
; Patent No. 5716930
; GENERAL INFORMATION:
; APPLICANT: Goodearl, Andrew; Stroobant, Paul;
; APPLICANT: Minghetti, Luisa; Waterfield, Michael; Marchioni, Mark;
; APPLICANT: Chen, Maio Su; Hiles, Ian
; TITLE OF INVENTION: Glial Mitogenic Factors, Their
; TITLE OF INVENTION: Preparation and Use
; NUMBER OF SEQUENCES: 184
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/249,322A
; FILING DATE: 26-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/036,555
; FILING DATE: 24-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/965,173
; FILING DATE: 23-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/940,389
; FILING DATE: 03-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/907,138
; FILING DATE: 30-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/863,703
; FILING DATE: 03-APRIL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.K. 91 07566.3
; FILING DATE: 10-APRIL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Tsai, Christine H.
; REGISTRATION NUMBER: 34,266
; REFERENCE/DOCKET NUMBER: LUD 250.4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 170:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 422
; TYPE: amino acid
; STRANDEDNESS:
;
; QY 2 RRGPSLRGRDAPAPTCVPAECFDLLVRHCVACGLLRTPRKPXAGASSPAP-----54
; DB 4 RRAPRR-SGRPGP-----RAQPGSAARSPPLPLPLLLL 38
;
; QY 55 --RTALQPOESVAGAGERAALPL-PGLLFGAPALLG-----LALVLALVLVGLVSWRRRQR 107
; DB 39 LGTAALAP-----GAAAGNEAAPAGASVCYSSPPSVGSVOELAQRAAAVIEGKVHPQRQQ 94
;
; QY 108 ---RLRGASSAEAP--DGDKDAPEPLDKVILSPGISDATAP-AWPPPGEDP-----GT 155
; DB 95 GALDRKAAAAGAGAGANGGDREPP-----AAGPRALGPAPAEPLLAANGT 139
;
; QY 156 TPGCHSVVPVA 166
; DB 140 VPSWPTAPVPS 150
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; RESULT 13
; US-08-428-926-3
; Sequence 3, Application US/08428926
; Patent No. 5667780
; GENERAL INFORMATION:
; APPLICANT: Ho, Wei-Hsien
; APPLICANT: Osheroff, Phyllis L.
; TITLE OF INVENTION: SENSORY AND MOTOR NEURON DERIVED FACTOR (SMDF)
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/428,926
; FILING DATE: 25-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/339517
; FILING DATE: 14-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 853D4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 422 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-428-926-3
;
; Query Match 12.2%; Score 118; DB 1; Length 422;
; Best Local Similarity 28.3%; Pred. No. 0.0045;
; Matches 54; Conservative 16; Mismatches 51; Indels 70; Gaps 11;
;
; QY 2 RRGPSLRGRDAPAPTCVPAECFDLLVRHCVACGLLRTPRKPXAGASSPAP-----54
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OM protein - protein search, using sw model

Run on: February 5, 2004, 17:56:29 ; Search time 13.125 Seconds
(without alignments)
1282.249 Million cell updates/sec

Title: US-10-045-574B-28

Perfect score: 907

Sequence: 1 MGARRLRVRSQRSDSSVPT.....PATELGSTELVTTKTAGPQ 175

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Pir1.*

2: Pir2.*

3: Pir3.*

4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	116.5	12.8	184	2 S43486	B-cell maturation
2	96	10.6	395	2 A43545	leukostatin CD43 p
3	96	10.6	395	2 I52842	CD43 Lp-3 antigen
4	94	10.4	1207	2 T00378	KIAA0641 protein -
5	92.5	10.2	563	2 C71529	hypothetical prote
6	88.5	9.8	910	2 A53137	tyrosine kinase re
7	85.5	9.4	339	2 S09264	Ig alpha chain C r
8	85.5	9.4	875	2 A49508	protein-tyrosine k
9	85.5	9.4	913	2 A48280	receptor tyrosine
10	85	9.4	378	2 S00842	leukostatin precu
11	85	9.4	1032	2 T34433	hypothetical prote
12	85	9.4	2232	2 T34434	hypothetical prote
13	84.5	9.3	246	2 PC4397	mucin 3 T10 - huma
14	84.5	9.3	2447	2 T16870	hypothetical prote
15	84	9.3	159	2 H75391	hypothetical prote
16	82.5	9.1	353	1 A1HU	Ig alpha-1 chain C
17	82.5	9.1	772	2 S32859	integrin beta 2 ch
18	82	9.0	416	1 JN0006	nerve growth facto
19	82	9.0	1459	2 T30196	kinesin motor prot
20	81.5	9.0	183	2 I59442	receptor tyrosine
21	81.5	9.0	220	2 T80329	receptor tyrosine
22	81.5	9.0	352	2 S05500	Ig alpha-1 chain C
23	81	8.9	3712	2 S18253	laminin alpha-1 ch
24	80.5	8.9	177	2 S25223	hypothetical 12.1
25	80	8.8	113	2 F65188	genome polypeptid
26	80	8.8	239	2 D82727	6-phosphoglucosola
27	80	8.8	293	2 G87018	probable membrane
28	80	8.8	356	2 S45330	thrombopoietin - m
29	80	8.8	748	2 S59327	hypothetical prote

30	79.5	8.8	240	2 F87537	TonB protein, prob
31	79.5	8.8	342	2 A45966	Ig alpha chain C r
32	79.5	8.8	855	2 H70910	hypothetical prote
33	79	8.7	262	2 C83434	translocation prot
34	79	8.7	400	1 A39822	leukostatin precu
35	79	8.7	620	2 A70525	hypothetical prote
36	78.5	8.7	369	2 S21471	genome polypeptid
37	78.5	8.7	636	1 VCVWFS	env polypeptid -
38	78	8.6	552	1 A31401	macrophage colony-
39	78	8.6	552	1 S35703	colony-stimulating
40	78	8.6	805	2 T49385	hypothetical prote
41	77.5	8.5	177	2 S32745	genome polypeptid
42	77.5	8.5	242	2 T49704	hypothetical prote
43	77.5	8.5	554	1 F70548	2-succinyl-6-hydro
44	77.5	8.5	770	2 B56695	transducin-like en
45	77.5	8.5	2237	2 T45115	N-type calcium cha

ALIGNMENTS

RESULT 1

S43486
B-cell maturation factor - human
N/Alternate names: BCM protein; BCM protein; BEL protein
C/Species: Homo sapiens (man)
C/Date: 27-Jan-1995 #sequence revision 27-Jan-1995 #text_change 21-Jul-2000
C/Accession: S43486; S31208; S36661
R/Laabi, Y.; Gras, M.P.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tsapis, A.
Nucleic Acids Res. 22, 1147-1154, 1994
A/Title: The BCM gene, preferentially expressed during B lymphoid maturation, is bidir
A/Reference number: S43486; MUID:94218235; PMID:8165126
A/Accession: S43486
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-184 <LAA>
A/Cross-references: EMBL:Z29574; NID:G471244; PIDN:CAA82690.1; PID:G471245
R/Laabi, Y.; Gras, M.P.; Carbone, F.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tsapis, EMO J. 11, 3897-3904, 1992
A/Title: A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene by a t(4;
A/Reference number: S31208; MUID:93010984; PMID:1396583
A/Accession: S31208
A/Molecule type: mRNA
A/Residues: 1-184 <LAA2>
A/Cross-references: EMBL:Z14954; NID:G29407; PIDN:CAA78679.1; PID:G29408
A/Accession: S36661
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 4-184 <LA3>
A/Cross-references: EMBL:Z14955
C/Genetics:
A/Gene: GDB:BCMA
A/Cross-references: GDB:135977; OMIM:109545
A/Map position: 16p13.1-16p13.1
A/Introns: 44/1; 93/1
C/Superfamily: human B-cell maturation factor

Query Match 12.8%; Score 116.5; DB 2; Length 184;

Best Local Similarity 29.4%; Pred. No. 0.0036;

Matches 50; Conservative 21; Mismatches 64; Indels 35; Gaps 8;

Qy 21 QCNQTECFDPLVRNCVSCELFHTPTDHTSSLEPGTALQPOEGSALRPDVALLVGAPALL 80

Db 7 QCSQNEVFDLLHACIPCOL-----RCSNTPTLTQRYCNASVTSVK---GTNAIL 56

Qy 81 GLTIALTVGLVSLVSWRWRQQLRTASPDTSVGQOE-----SLENVFPSSSE-- 129

Db 57 WTCIGLSLI--ISLAVFVLMFLRKIS---SEPLKDEFNKTSGLLGANIDLEKSRIGD 111

Qy 130 ----PHASAPTFWPLK-EDADSALPR----HSVPVPATELGSTELVTTKT 170

Db 112 EIIPLRGLEVTVECTCEDCIKSKPKVDSDHCFPLPAMEGATILVTTKT 161

Query March 10.6%; Score 96; DB 2; Length 395;
Best Local Similarity 33.7%; Pred. No. 0.56;
Superfamily: leukosialin

Matches	47;	Conservative	19;	Mismatches	48;	Indels	65;	Gaps	11;
QY	35	CVSCELFT	-----EDTGH-----	TSSLEPGYALQPGSALRPDVA	LLVGPAL	79			
Db	76	CVACHVEHNDYRLILFCPDTHSSCPPTSCGRPSLSQ	-----RPDLRDLILGSDA-	127					
QY	80	LGLILALTLGLV	---SLVSWRWQQLRTASPDTSSEGVQOESLEN	---VFVPSSETHEA	132				
Db	128	---SLTCTLRGLKPKDKDAVFTWE	-----PTNGNEPVQOSFQDPDCCCYSVSSVLP	-G 175					
QY	133	SAPTW	-----PPLKEDADSALPR--HSVPVPATELGSTELVT	167					
Db	176	CAETWTAGTEFTCTWTHPEIEGSSLTATIRKDTGSLTPQVHLLPPPSBELAINALVT	233						

RESULT 8
 A49508
 protein-tyrosine kinase (EC 2.7.1.112) trkE precursor - human
 C;Species: Homo sapiens (man)
 C;Date: 10-Nov-1995 #sequence revision 10-Nov-1995 #text_change 04-Feb-2000
 C;Accession: A49508; I38358; S37402
 R;Di Marco, E.; Cutuli, N.; Guerra, L.; Cancedda, R.; De Luca, M.
 J. Biol. Chem. 268, 24290-24295, 1993
 A;Title: Molecular cloning of trkE, a novel trk-related putative tyrosine kinase receptor
 A;Reference number: A49508; MUID:94043265; PMID:8226377
 A;Accession: A49508
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-876 <DIA>
 C;Cross-references: EMBL:X74979; NID:g400462; PIDN:CAAS2915.1; PID:g400463
 C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; discoidin I amino-te-
 C;Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase
 F;30-185/Domain: discoidin I amino-terminal homology <DN1>
 F;571-875/Domain: protein kinase homology <KIN>
 F;579-587/Region: protein kinase ATP-binding motif

Query Match	9.4%;	Score	85.5;	DB	2;	Length	876;
Best Local Similarity	30.2%;	Pred. No.	12;				
Matches	39;	Conservative	19;	Mismatches	38;	Indels	33;
Gaps	10;						

QY 44 PDTGHTSLEPGTALQPO-----EGSALRPDVALLVGAPALGLIILALTLVGLVSLV 95
 Db 390 PPTTWFSLE-----LEPRGQPVAKAES-----PTAILIG-CLVAIIILLLI--IALM 437

QY 96 SWR--WRQQLRTASPDTSSEGVQOESLENVFVPS-----SETHASAPTWPPLKEDADSAL 148
 Db 438 LRLHWRLLSKAE--RRVLEELTVHLSVPGDTILINNRPGPREP--PPYQEPRPGRN 492

QY 149 PRHSVP-VP 156
 Db 493 PPHSAPCPV 501

RESULT 9
 A48280
 receptor tyrosine kinase - human
 C;Species: Homo sapiens (man)
 C;Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 24-Sep-1999
 C;Accession: A48280
 R;Johnson, J.D.; Edman, J.C.; Rutter, W.J.
 Proc. Natl. Acad. Sci. U.S.A. 90, 5677-5681, 1993
 A;Title: A receptor tyrosine kinase found in breast carcinoma cells has an extracellular
 A;Reference number: A48280; MUID:93296201; PMID:8390675
 A;Accession: A48280
 A;Status: preliminary; translated from GB/EMBL/DBD
 A;Molecule type: mRNA
 A;Residues: 1-913 <RES>
 A;Cross-references: GB:LI1315; NID:g403386; PIDN:AAA02866.1; PID:g403387
 C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; discoidin I amino-te-
 C;Keywords: ATP
 F;30-185/Domain: discoidin I amino-terminal homology <DN1>
 F;608-912/Domain: protein kinase homology <KIN>
 F;616-624/Region: protein kinase ATP-binding motif

Query Match 9.4%; Score 85.5; DB 2; Length 913;
Best Local Similarity 30.2%; Pred. No. 12;
Matches 39; Conservative 19; Mismatches 38; Indels 33; Gaps 10;

QY 44 PTHGTSLEPGTALQPO-----RGSALRDPDVALVGCAPALLGLILALTLVGLVSLV 95
DB 390 PPTNFSSLE-----LEPRGQFVAKAGS-----PTALIG--CLVAIIILLILI--IALM 437
QY 96 SWR--WRQRLTASPTDSEGVQESLENVFPVS-----SETPHASAPTWPPLKEDADSAL 148
DB 438 LWRLHWRLLSKAE--RRVLEBELTVHLSVPGDTIILNNRPGRP--PPYQEPREPCN 492
QY 149 PHSVP-VP 156
DB 493 PPHSAPCPV 501

RESULT 10
S00842
leukosialin precursor - rat (fragment)
N;Alternate names: leucocyte sialoglycoprotein; sialoprophorin
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 23-Jul-1999
C;Accession: S00842
R;Killeen, N.; Barclay, A.N.; Wallis, A.C.; Williams, A.F.
EMBO J. 5, 4029-4034, 1987
A;Title: The sequence of rat leukosialin (W3/13 antigen) reveals a molecule with O-linked
F;1-7/Domain: signal sequence #status predicted <SIG>
F;8-378/Product: leukosialin #status predicted <MAT>

Query Match 9.4%; Score 85; DB 2; Length 378;
Best Local Similarity 24.1%; Pred. No. 5.1;
Matches 48; Conservative 19; Mismatches 74; Indels 58; Gaps 7;

QY 14 RDSSVP--TQCNTCECPDPLVNCVSELFTPTDGTHTSSLEPG----- 55
DB 137 KGTSAAPPVTVTSSTGTFVATTVSSETSGPPVTMATGSLGPSKETHGLSATIATSSGE 196
QY 56 -----TALQPOEGSALRDPDVALVGCAPALLGLILALTLVGL 91
DB 197 SSVAGGTFVFSKISTSTNPITVTPPRGSS-----GMLLYS--MLIALTVLVIVL 250
QY 92 VSLVSWRQQLRTASPTDSEGVQESLENVFPVSSETPHASAPTWPPLKEDADSALPRH 151
DB 251 --LLWROQKERTGALTLSRGKNGTVDWAGPARVPDEEATT-----ASGSGGNK 301
QY 152 VSPVPATELGSLELVTTTKT 170
DB 302 SSGAPETD-GSQRPFLIT 319

RESULT 11
T34433
hypotheical protein K06A9.1a - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 18-Feb-2000
C;Accession: T34433
R;Geisel, C.; Gattung, S.
submitted to the EMBL Data Library, December 1996
A;Description: The sequence of C. elegans cosmid K06A9.
A;Reference number: Z21525
A;Accession: T34433
A;Status: Preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1032 <GEI>

A;Cross-references: EMBL:U80846; PIDN:AAC70893.1; GSPDB:GN00028; CESP:K06A9.1a
A;Experimental source: strain Bristol N2; clone K06A9
C;Genetics:
A;Gene: CESP:K06A9.1a
A;Map position: X
A;Introns: 38/1; 75/3; 103/3; 132/2; 158/2; 222/3; 839/1; 849/1; 875/3; 940/2; 966/2; 9

Query Match 9.4%; Score 85; DB 2; Length 1032;
Best Local Similarity 28.2%; Pred. No. 16;
Matches 37; Conservative 18; Mismatches 48; Indels 28; Gaps 7;

QY 46 TGTSSLEPGTALQPOEGSALRDPDVALVGCAPALLGLILALTLVGLVSLVSWRQQLRT 105
DB 515 TGTSTVTPGSGSTSPAPSSPNPS-----SSPASTG--STITISGSSII-----VST 560
QY 106 ASPDT---SEGVOQESLENVFPVSSETPHASAPTWPPLKEDADSALPRHSVPVPATELGS 162
DB 561 VSGSTVSGSTGTSTQSTLAS----STATP-GSSSTVP-----SSSPQSPSSQSPAPNTGS 609
QY 163 TELVTTKTACP 173
DB 610 TTPSQTSQSP 620

RESULT 12
T34434
hypotheical protein K06A9.1a - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 18-Feb-2000
C;Accession: T34434
R;Geisel, C.; Gattung, S.
submitted to the EMBL Data Library, December 1996
A;Description: The sequence of C. elegans cosmid K06A9.
A;Reference number: Z21525
A;Accession: T34434
A;Status: Preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-2232 <GEI>
A;Cross-references: EMBL:U80846; PIDN:AAC70890.1; GSPDB:GN00028; CESP:K06A9.1a
A;Experimental source: strain Bristol N2; clone K06A9
C;Genetics:
A;Gene: CESP:K06A9.1a
A;Map position: X
A;Introns: 38/1; 75/3; 103/3; 132/2; 158/2; 222/1; 1088/1; 1367/1; 2039/1; 2049/1; 2075

Query Match 9.4%; Score 85; DB 2; Length 2232;
Best Local Similarity 28.2%; Pred. No. 38;
Matches 37; Conservative 18; Mismatches 48; Indels 28; Gaps 7;

QY 46 TGTSSLEPGTALQPOEGSALRDPDVALVGCAPALLGLILALTLVGLVSLVSWRQQLRT 105
DB 515 TGTSTVTPGSGSTSPAPSSPNPS-----SSPASTG--STITISGSSII-----VST 560
QY 106 ASPDT---SEGVOQESLENVFPVSSETPHASAPTWPPLKEDADSALPRHSVPVPATELGS 162
DB 561 VSGSTVSGSTGTSTQSTLAS----STATP-GSSSTVP-----SSSPQSPSSQSPAPNTGS 609
QY 163 TELVTTKTACP 173
DB 610 TTPSQTSQSP 620

RESULT 13
PC4397
mucin 3 T10 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 10-Nov-1997 #sequence_revision 10-Nov-1997 #text_change 08-Oct-1999
C;Accession: PC4397
R;Van Klippen, B.J.W.; Van Dijken, T.C.; Oussoren, E.; Bueller, H.A.; Dekker, J.; Einer
Biochem. Biophys. Res. Commun. 238, 143-148, 1997
A;Title: Molecular cloning of human MUC3 cDNA reveals a novel 59 amino acid tandem repe
A;Reference number: PC4395; MUID:97445141; PMID:9299468
A;Accession: PC4397

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 5, 2004, 17:49:49 ; Search time 9.72222 Seconds
(without alignments)
846.481 Million cell updates/sec

Title: US-10-045-574B-28

Perfect score: 907

Sequence: 1 MGARRLRVRSQSRDSSVPT.....PATELGSTELVTKTAGPEQ 175

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	907	100.0	175	1	T13C MOUSE
2	410.5	45.3	184	1	T13C HUMAN
3	116.5	12.8	184	1	TR17 MOUSE
4	101.5	11.2	185	1	TR17 MOUSE
5	96	10.6	395	1	LEUK MOUSE
6	88.5	9.8	910	1	DDRI RAT
7	87.5	9.6	911	1	DDRI MOUSE
8	87.5	9.6	2863	1	LRBA HUMAN
9	85.5	9.4	913	1	DDRI HUMAN
10	85	9.4	378	1	LEUK RAT
11	83	9.2	407	1	ADRM MOUSE
12	82.5	9.1	353	1	ALCI HUMAN
13	82.5	9.1	520	1	PKN2 COREF
14	82	9.0	416	1	TR16 CHICK
15	81.5	9.0	353	1	ALCI GORGO
16	81	8.9	407	1	ADRM RAT
17	81	8.9	429	1	COBB RHIME
18	81	8.9	745	1	METE CORGL
19	81	8.9	2472	1	NCR2 MOUSE
20	81	8.9	3712	1	LMA DROME
21	80	8.8	239	1	6PGL XLYFA
22	80	8.8	356	1	TPO MOUSE
23	79	8.7	400	1	LEUK HUMAN
24	78.5	8.7	636	1	ENV MCFP
25	78	8.6	552	1	CSFI MOUSE
26	77.5	8.5	933	1	PRGR HUMAN
27	77.5	8.5	1253	1	SHK2 HUMAN
28	77.5	8.5	2090	1	HFC1 MSAU
29	77	8.5	92	1	PLM CANFA
30	77	8.5	249	1	TN12 HUMAN
31	76.5	8.4	256	1	TIPA PHAVU
32	76.5	8.4	476	1	PKNF MYCTU
33	76.5	8.4	5703	1	MUSE_HUMAN

34 76 8.4 897 1 CYRB HUMAN
35 76 8.4 1255 1 PER2 HUMAN
36 76 8.4 3726 1 ABP1 MOUSE
37 75.5 8.3 457 1 BAG4 HUMAN
38 75.5 8.3 912 1 PGCB BOVIN
39 75.5 8.3 1187 1 A11A MOUSE
40 75.5 8.3 1364 1 NTC4 MOUSE
41 75.5 8.3 2321 1 NTC3 HUMAN
42 75 8.3 404 1 RAGE BOVIN
43 75 8.3 416 1 RAGE BOVIN
44 75 8.3 920 1 AD19 MOUSE
45 75 8.3 982 1 CRM_DROME

ALIGNMENTS

RESULT 1
T13C_MOUSE
ID T13C_MOUSE STANDARD; PRT; 175 AA.
AC QSD8D0;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 13C (B cell-
activating factor receptor) (BAFF receptor) (BAFF-R) (Blys receptor
3) (B-cell maturation defect).
DE TNFRSF13C OR BAFFR OR BCMD OR BR3.
GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC STRAIN=BALE/c; TISSUE=B-cell lymphoma;
RX MEDLINE=21442025; PubMed=11509692;
RA Thompson J.S., Bixler S.A., Qian F., Vora K., Scott M.L.,
Cachero T.G., Hession C., Schneider P., Sizing I.D., Mullen C.,
Strauch K., Zafari M., Benjamin C.D., Tschopp J., Browning J.L.,
Ambrose C.;
RA "BAFF-R, a newly identified TNF receptor that specifically interacts
with BAFF".
RL Science 293:2108-2111(2001).
[2]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND DISEASE.
RC STRAIN=A/J;
RX MEDLINE=21475520; PubMed=11591325;
RA Yan M., Brady J.R., Chan B., Lee W.P., Hsu B., Harless S.M.,
Cancro M.P., Grewal I.S., Dixit V.M.;
RA "Identification of a novel receptor for B lymphocyte stimulator that
is mutated in a mouse strain with severe B cell deficiency".
RL Curr. Biol. 11:1547-1552(2001).
[3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC STRAIN=C57BL/6J; TISSUE=Small intestine;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itch M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yananaka I.,
Saito T., Okazaki Y., Gotojori T., Bono H., Kasukawa T., Saito R.,
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
Schiraldi L.M., Staubl F., Suzuki R., Tomita M., Wagner L., Washio T.,
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Suzuki H., Toyooka K., Wang K.H., Weiss C., Whittaker C., Wilming L.,
Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RN Nature 409:685-690(2001).
 RP FUNCTION.
 RX MEDLINE=21614654; PubMed=11747827;
 RA Harless S.M., Lentz V.M., San A.F., Hsu B.L., Clise-Dwyer K.,
 Hilbert D.M., Hayes C.E., Cancro M.P.;
 RT "Competition for B-lymphocyte mediated signaling through Bcnd/BR3 regulates
 peripheral B lymphocyte numbers.";
 RL Curr. Biol. 11:1986-1989(2001).
 CC -!- FUNCTION: B-cell receptor specific for TNFSF13B/TALL1/BAFF/BLYS.
 CC Promotes the survival of mature B-cells and the B-cell response.
 CC -!- SUBCELLULAR LOCATION: Type III membrane protein (Probable).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=Q9D8D0-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q9D8D0-2; Sequence=VSP_006506;
 CC -!- TISSUE SPECIFICITY: Highly expressed in spleen and testis;
 CC detected at lower levels in lung and thymus.
 CC -!- DISEASE: Defects in TNFSF13C are a cause of severe B-cell
 CC deficiency. B-cell deficient strain A/WySnJ has a 4.7 kb insertion
 CC in the BAFFR gene leading to an altered C-terminus. The mutant RNA
 CC is not detectable. B-cell lymphoproliferation is normal, but the life
 CC span of peripheral B-cells is much reduced.
 CC -!- SIMILARITY: Contains 1 TNFR-Cys repeat.
 CC -----
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 CC -----
 CC EMBL; AF373847; AAK91827.1; -;
 CC EMBL; AK008142; BAB25490.1; -;
 CC MGD; MGI:191299; Tnftrf13c.
 DR Receptor; Immune response; Signal-anchor; Transmembrane; Glycoprotein;
 KW Alternative splicing;
 FT DOMAIN 1 71 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 72 92 SIGNAL-ANCHOR
 FT DOMAIN 93 175 CYTOPLASMIC (POTENTIAL).
 FT REPEAT 21 38 TNFR-CYS (PARTIAL).
 FT DISULFID 22 35 BY SIMILARITY.
 FT DISULFID 27 38 BY SIMILARITY.
 FT CARBOHYD 23 23 N-LINKED (GLCNAC...) (POTENTIAL).
 FT VARSPPLIC 133 143 Missing (in isoform 2).
 FT SEQUENCE 175 AA; 18798 MW; 28BC7C1A02FB87EF CRC64;
 Query Match 100.0%; Score 907; DB 1; Length 175;
 Best Local Similarity 100.0%; Pred. No. 1.3e-71;
 Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGARLRVRSQRSDSSVPTQCNTECFDPLVRNCVSCELFHTPDGTGHTSSLEPGTALQP 60
 DB 1 MGARLRVRSQRSDSSVPTQCNTECFDPLVRNCVSCELFHTPDGTGHTSSLEPGTALQP 60
 QY 61 QEGSALRPDVALVCGAPALLGLIALTLVGLVLSVSWRQQLRTASPDTSSEGVQGESLE 120
 DB 61 QEGSALRPDVALVCGAPALLGLIALTLVGLVLSVSWRQQLRTASPDTSSEGVQGESLE 120
 QY 121 NVFVPSSTPHASPTWPFPLKEDADSLPRHSVPVPATLGSTELVTTKTAGEPQ 175
 DB 121 NVFVPSSTPHASPTWPFPLKEDADSLPRHSVPVPATLGSTELVTTKTAGEPQ 175
 RESULT 2
 T13C_HUMAN

TD T13C_HUMAN STANDARD; PRT; 184 AA.
 AC Q96RJ3;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 13C (B cell-
 DE activating factor receptor) (BAFF-R) (BLYS receptor
 3).
 GN TNFSF13C OR BAFFR OR BR3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC TISSUE=B-cell lymphoma;
 RX MEDLINE=21442025; PubMed=11509692;
 RA Thompson J.S., Bixler S.A., Qian F., Vora K., Scott M.L.,
 Cachero T.G., Hession C., Schneider P., Sizing I.D., Muller C.,
 Strauch K., Zafari M., Benjamin C.D., Tschopp J., Browning J.L.,
 Ambrose C.;
 RA "BAFF-R, a newly identified TNF receptor that specifically interacts
 RT with BAFF.";
 RL Science 293:2108-2111(2001).
 RN [2]
 RP FUNCTION.
 RX MEDLINE=21475520; PubMed=11591325;
 RA Yan M., Brady J.R., Chan B., Lee W.P., Hsu B., Harless S.M.,
 Cancro M.P., Grewal I.S., Dixit V.M.;
 RT "Identification of a novel receptor for B lymphocyte stimulator that
 RT is mutated in a mouse strain with severe B cell deficiency.";
 RL Curr. Biol. 11:1547-1552(2001).
 CC -!- FUNCTION: B-cell receptor specific for TNFSF13B/TALL1/BAFF/BLYS.
 CC Promotes the survival of mature B-cells and the B-cell response.
 CC -!- SUBCELLULAR LOCATION: Type III membrane protein (Probable).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=Q96RJ3-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q96RJ3-2; Sequence=VSP_006505;
 CC Note=No experimental confirmation available;
 CC -!- TISSUE SPECIFICITY: Highly expressed in spleen and lymph node, and
 CC in resting B-cells. Detected at lower levels in activated B-cells,
 CC resting CD4+ T-cells, in thymus and peripheral blood leukocytes.
 CC -!- SIMILARITY: Contains 1 TNFR-Cys repeat.
 CC -----
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 CC -----
 CC EMBL; AF373846; AAK91826.1; -;
 CC PD3; IMPV; 30-OCT-02.
 CC Genew; HGNC:17755; TNFSF13C.
 CC MIM; 606269; -;
 CC InterPro; IPR001369; TNFR_C6.
 CC PROSITE; PS00652; TNFR_NGFR.1; FALSE NEG.
 CC PROSITE; PS00650; TNFR_NGFR.2; FALSE NEG.
 CC Receptor; Immune response; Signal-anchor; Transmembrane;
 CC Alternative splicing; 3D-structure.
 FT DOMAIN 1 78 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 79 99 SIGNAL-ANCHOR
 FT DOMAIN 100 184 (TYPE III MEMBRANE PROTEIN) (POTENTIAL).
 FT REPEAT 18 35 TNFR-CYS (PARTIAL).
 FT DISULFID 19 32 BY SIMILARITY.
 FT DISULFID 24 35 BY SIMILARITY.
 FT VARSPPLIC 143 143 P -> PA (in isoform 2).
 FT SEQUENCE 184 AA; 18798 MW; 28BC7C1A02FB87EF CRC64;

SQ SEQUENCE 184 AA; 18863 MW; F28FB9809A27138 CRC64;
Query Match 45.3%; Score 410.5; DB 1; Length 184;
Best Local Similarity 56.1%; Pred. No. 1.1e-28;
Matches 101; Conservative 9; Mismatches 55; Indels 15; Gaps 6;
QY 9 RSORSDDSSVPTCCNTECFDPLVNCVSCLEFHT--PDTGHTSLERPGTALQPC----- 62
DB 6 RSURGDAPAFPCVPAECFDLVRHCVACGLRPRPKPAGASSPAPRTALQPCESVGA 65
QY 63 --GSALRPDVALLVGAPALLGLILALTILVGLVSLVSWRWQ-QLTAS-----PPTSQGVQ 115
DB 66 GAGEAALPLGLLFGAPALLGLALVLAIV-LVGLVSWRRQRRLRGASSARAPGDKDA- 123
QY 116 QESLENVFPSSSTPHASAPTPPPLKEDADSLPHSVDPVATELGSTELVTTKTAPEQ 175
DB 124 PEPLDKVILSPGISDATAPAWPPPGEDGTTTPGHSVPEVATELGSTELVTTKTAPEQ 183
RESULT 3
TR17_HUMAN
ID TR17_HUMAN STANDARD; PRT; 184 AA.
AC Q02223;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 17 (B-cell
maturation protein).
GN TNFRSF17 OR BCMA OR BCM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI TaxID=9606;
[1]
RN SEQUENCE FROM N.A., AND CHROMOSOMAL TRANSLOCATION.
RC TISSUE=Lymph node, and Peripheral blood leukocytes;
RX MEDLINE=93010984; PubMed=1396583;
RA Laabi Y., Gras M.P., Carbonnel F., Brouet J.C., Berger R.,
RA Larsen C.J., Tsapis A.;
RT "A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene
by a t(4;16)(q26;p13) translocation in a malignant T cell lymphoma.";
RL EMO J. 11:3897-3904(1992).
[2]
RN SEQUENCE FROM N.A.
RX MEDLINE=94218235; PubMed=8165126;
RA Laabi Y., Gras M.P., Brouet J.C., Berger R., Larsen C.J., Tsapis A.;
RT "The BCMA gene, preferentially expressed during B lymphoid
maturation, is bidirectionally transcribed.";
RL Nucleic Acids Res. 22:1147-1154(1994).
[3]
RN SEQUENCE FROM N.A.
RX MEDLINE=99425270; PubMed=10493829;
RA Loftus B.J., Kim U.-J., Shedd V.P., Kalush F., Brandon R.,
RA Fuhrmann J., Mason T., Crosby M.L., Barnstead M., Cronin L.,
RA Deslattes Mays A., Cao Y., Xu R.X., Kang H.-L., Mitchell S.,
RA Eichler E.E., Harris P.C., Venter J.C., Adams M.D.;
RT "Genome duplications and other features in 12 Mb of DNA sequence from
human chromosome 16p and 16q.";
RL Genomics 60:295-308(1999).
[4]
RN SEQUENCE FROM N.A., AND VARIANT THR-153.
RX MEDLINE=21419161; PubMed=11528522;
RA Kawasaki A., Tsuchiya N., Fukazawa T., Hashimoto H., Tokunaga K.;
RT "Presence of four major haplotypes in human BCMA gene: lack of
association with systemic lupus erythematosus and rheumatoid
arthritis.";
RL Genes Immun. 2:276-279(2001).
[5]
RN FUNCTION, AND INTERACTION WITH TRAF1 AND TRAF3.
RX MEDLINE=20363816; PubMed=10903733;
RA Hatzoglou A., Rousset J., Bourgeade M.-F., Rogier E., Madry C.,
RA Inoue J.-I., Devergne O., Tsapis A.;
RT "TNF receptor family member BCMA (B cell maturation) associates with

TNF receptor-associated factor (TRAF) 1, TRAF2, and TRAF3 and
RT activates NF-kappa B, elk-1, c-Jun N-terminal kinase, and p38
RT mitogen-activated protein kinase.";
RL J. Immunol. 165:1322-1330(2000).
[6]
RN FUNCTION.
RX MEDLINE=20259066; PubMed=10801128;
RA Gross J.A., Johnston J., Mudri S., Enselman R., Dillon S.R.,
RA Madden K., Xu W., Parrish-Novak J., Foster D., Lofton-Day C.,
RA Moore M., Littau A., Grossman A., Haugen H., Foley K., Blumberg H.,
RA Harrison K., Kindsvogel W., Clegg C.H.;
RT "TAC1 and BCMA are receptors for a TNF homologue implicated in B-cell
autoimmune disease.";
RL Nature 404:995-999(2000).
[7]
RN FUNCTION, AND INTERACTION WITH APRIL AND BAFF.
RX MEDLINE=21170294; PubMed=10973284;
RA Yu G., Boone T., Delaney J., Hawkins N., Kelley M., Ramakrishnan M.,
RA McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stolina M.,
RA Boyle W.J., Sarosi I., Hsu H., Senaldi G., Theill L.E.;
RT "APRIL and TALL-1 and receptors BCMA and TACI: system for regulating
humoral immunity.";
RL Nat. Immunol. 1:252-256(2000).
[8]
RN INTERACTION WITH TRAF5 AND TRAF6.
RX MEDLINE=20381353; PubMed=10908663;
RA Shu H.-B., Johnson H.;
RT "B cell maturation protein is a receptor for the tumor necrosis factor
family member TALL-1.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:9156-9161(2000).
CC -1- FUNCTION: Receptor for TNFSF13B/SLyS/BAFF and TNFSF13/APRIL.
CC Promotes B-cell survival and plays a role in the regulation of
CC humoral immunity. Activates NF-kappa-B and JNK.
CC -1- SUBUNIT: Associates with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6.
CC -1- SUBCELLULAR LOCATION: Type III membrane protein. Plasma membrane
CC and perinuclear Golgi-like structures.
CC -1- TISSUE SPECIFICITY: Expressed in mature B-cells, but not in T-
CC cells or monocytes.
CC -1- DISEASE: A FORM OF T-CELL ACUTE LYMPHOBLASTIC LEUKEMIA (T-ALL) IS
CC CHARACTERIZED BY A CHROMOSOMAL TRANSLOCATION T(4;16)(Q26;P13)
CC WHICH INVOLVES BCMA AND IL2.
CC -1- SIMILARITY: Contains 1 TNFR-Cys repeat.
CC
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EMBL; Z14954; CAA78679.1; -;
DR EMBL; Z29575; CAA82691.1; -;
DR EMBL; Z29574; CAA82690.1; -;
DR EMBL; U95742; AAB67251.1; -;
DR EMBL; AB052772; BAB60895.1; -;
DR PIR; S43486; S43486.1; -;
DR Genbank; HGNC:11913; TNFRSF17.
DR MIM; 109545; -;
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0005886; C:plasma membrane; TAS.
DR GO; GO:0004872; F:receptor activity; TAS.
DR GO; GO:0008283; P:cell proliferation; TAS.
DR GO; GO:0007275; P:development; TAS.
DR GO; GO:0007165; P:signal transduction; TAS.
DR Receptor; Immune response; Proto-oncogene; Signal-anchor;
KW Transmembrane; Chromosomal translocation; Polymorphism.
FT DOMAIN 1 54
FT SIGNAL-ANCHOR (TYPE III MEMBRANE PROTEIN)
FT TRANSMEM 55 77
FT (POTENTIAL).
FT DOMAIN 78 184
FT CYTOPLASMIC (POTENTIAL).
FT REPEAT 7 41
FT TNFR-CYS
FT BREAKPOINT FOR TRANSLOCATION TO FORM
FT SITE

INTERLEUKIN 2/BCM ONCOGENE.

DISULFID 8 21
FT BY SIMILARITY.
FT DISULFID 24 37
FT BY SIMILARITY.
FT DISULFID 28 41
FT BY SIMILARITY.
FT VARIANT 153
FT A -> T.
FT /FTID=VAR_012234.
SQ SEQUENCE 184 AA; 20138 MW; 277AF11E2767D932 CRC64;

Query Match 12.8%; Score 116.5; DB 1; Length 184;
Best Local Similarity 29.4%; Pred. No. 0.0029;
Matches 50; Conservative 21; Mismatches 64; Indels 35; Gaps 8;
QY 21 QCNTECPDPLVRNCVSCELFHTPTDGTSSLEPGTALQPGSALRPDPVALLVAPALL 80
Db QCSQNEVFDSLHACIPCOL-----RCSNTPPLTCQRYCNASVTNSVK---GTNAIL 56
QY 81 GLILALTALVGLVSLVSWRQQLRTASPDTSSEGVQOE-----SLENVFPVPSSET-- 129
Db 57 WTCIGLSLI--ISLAVFVLMFLKKIS---SEPLKDEFTKGTGGLGMANIDLEKSRGD 111
QY 130 ----PHASAPTWPLK-EDADSALPR-----HSVPVPATELGSTELVTTKT 170
Db 112 EILLPRGLETVETECTDCIKSPKVDSDHCFLPAMERGATILVTTKT 161

RESULT 4

TR17 MOUSE
ID TR17 MOUSE STANDARD; PRT; 185 AA.
AC O88472;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 17 (B-cell
DE maturation protein).
GN TNFRSF17 OR BCMA OR BCM.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1 AND 2).
RX STRAIN=C57BL/6J; TISSUE=Spleen;
RX MEDLINE=99061155; PubMed=9846698;
RA Madry C., Laabi Y., Callebaut I., Roussel J., Hatzoglou A.,
RA Le Coniat M., Mornon J.P., Berger R., Teapic A.;
RT "The characterization of murine BCMa gene defines it as a new member
RT of the tumor necrosis factor receptor superfamily.";
RL Int. Immunol. 10:1693-1702(1998).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX STRAIN=C57BL/6J; TISSUE=Colon;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.P.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Sava T., Shibata Y., Storch K.-F.,
RA Suzuki H., Tovo-Oka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -1- FUNCTION: Receptor for TNFSF13B/BLys/BAPF and TNFSF13/APRIL.

Promotes B-cell survival and plays a role in the regulation of humoral immunity. Activates NF-kappa-B and JNK (By similarity).
-1- SUBUNIT: Associates with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6 (By similarity).
-1- SUBCELLULAR LOCATION: Type III membrane protein (Probable).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=O88472-1; Sequence=Displayed;
CC Name=2;
CC IsoId=O88472-2; Sequence=VSP_006507;
CC -1- TISSUE SPECIFICITY: Detected in spleen, thymus, bone marrow and heart, and at lower levels in kidney and lung.
CC -1- SIMILARITY: Contains 1 TNFR-Cys repeat.
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EMBL; AF061505; AAC23799.1; -;
EMBL; AK020247; BAB32038.1; -;
MCD; MGI:1343050; Tnf1sf17.
KW Receptor; Immune response; Signal-anchor; Transmembrane;
FT DOMAIN 1 49
FT TRANSMEM 50 70
FT SIGNAL-ANCHOR
FT TYPE III MEMBRANE PROTEIN (POTENTIAL).
FT EXTRACELLULAR (POTENTIAL).
FT CYTOPLASMIC (POTENTIAL).
FT TNFR-CYS.
FT BY SIMILARITY.
FT DISULFID 4 36
FT DISULFID 5 18
FT DISULFID 21 32
FT DISULFID 25 36
FT VARSPLIC 87 91
FT Missing (in isoform 2).
FT /FTID=VSP_006507.
SQ SEQUENCE 185 AA; 20442 MW; 8806352B4FD26A8E CRC64;

Query Match 11.2%; Score 101.5; DB 1; Length 185;
Best Local Similarity 29.4%; Pred. No. 0.057;
Matches 53; Conservative 14; Mismatches 60; Indels 53; Gaps 9;
QY 21 QCNTECPDPLVRNCVSCELFHTPTDGTSSLEPGTALQPGSALRPDPVALLV-GAPAL 79
Db 4 QCFHSEYFDSLHACKPC-----HLRCSNPPATCQFY----CDPSVTSSVKGTVTV 50

QY 80 LGLILALTALVGLVSL--VSWRQQLRTA-----SPDTSEGVQO----- 116
Db 51 LMIFLGLTLVLSLALFTISFLRKMPEALKDEPQPGQLDGSALDKADTELTRIRAGD 110
QY 117 -----ESLE-NVFPVPSSETPHASAPTWPLKEDADSALPRHSVPVPATELGSTELVTTKT 170
Db 111 DRIFPRSLRYETVECTDCVKSKEP-----KGDS-----HFFPLPAMEGATILVTTKT 160

RESULT 5

LEUK MOUSE
ID LEUK MOUSE STANDARD; PRT; 395 AA.
AC P15702;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Leukostatin precursor (Bucocyte stialoglycoprotein) (Sialophorin)
DE (CD43 antigen) (L4 48) (B cell differentiation antigen Lp-3).
GN SPN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=DRB/2J; TISSUE=Liver;
RX MEDLINE=90269342; PubMed=2347365;
RA Cyster J.G., Somoza C., Killen N., Williams A.F.;
RT "Protein sequence and gene structure for mouse leukosialin (CD43), a
RL T lymphocyte mucin without introns in the coding sequence.";
RL Eur. J. Immunol. 20:875-881(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=B10.P; TISSUE=Liver;
RX MEDLINE=90370495; PubMed=2144340;
RA Dorfman K.S., Litaker K.S., Baecher C.M., Frelinger J.G.;
RT "The nucleotide sequence of Ly 48 (mouse leukosialin, sialophorin):
RL the mouse homolog of CD43.";
RL Nucleic Acids Res. 18:4932-4932(1990).
RN [3]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=94236703; PubMed=7514104;
RA Shioita J., Nishimura H., Okamoto H., Yu B., Hattori S., Abe M.,
RA Okada T., Nozawa S., Tsurui H., Hirose S.;
RT "A unique murine CD43 epitope Lp-3: distinct distribution from
RL another CD43 epitope 87.";
RL Cell. Immunol. 155:402-413(1994).
RN [4]
RP SEQUENCE OF 345-383 FROM N.A.
RX STRAIN=C57BL/6J;
RX MEDLINE=90316596; PubMed=1973410;
RA Baecher C.M., Dorfman K.S., Mattei M.-C., Frelinger J.G.;
RT "cDNA cloning and localization of the mouse leukosialin gene (Ly48)
RL to chromosome 7.";
RL Immunogenetics 31:307-314(1990).
RN [5]
RP BINDING TO SN.
RX MEDLINE=21136329; PubMed=11238599;
RA van den Berg T.K., Nath D., Ziltener H.J., Vestweber D., Fukuda M.,
RA "CD43 functions as a T cell counterreceptor for the macrophage
RT adhesion receptor sialoadhesin (Siglec-1).";
RL J. Immunol. 166:3637-3640(2001).
RN [6]
RP FUNCTION.
RX MEDLINE=21585789; PubMed=11728336;
RA Allenspach E.J., Cullinan P., Tong J., Tang Q., Tesciuba A.G.,
RA Cannon J.B., Takahashi S.M., Morgan R., Burkhardt J.K., Sperling A.I.;
RT "ERK-dependent movement of CD43 defines a novel protein complex distal
RL to the immunological synapse.";
RL Immunity 15:739-750(2001).
CC -!- FUNCTION: One of the major glycoproteins of thymocytes and T
CC lymphocytes. Plays a role in the physicochemical properties of the
CC T-cell surface and in lectin binding. Presents carbohydrate
CC ligands to selectins. Has an extended rodlike structure that could
CC protrude above the glycocalyx of the cell and allow multiple
CC glycan chains to be accessible for binding. Is a counterreceptor
CC for SN/Siglec-1. During T-cell activation is actively removed from
CC the T-cell-APC (antigen-presenting cell) contact site thus
CC suggesting a negative regulatory role in adaptive immune response.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Cell surface of thymocytes, T lymphocytes,
CC neutrophils, plasma cells and myelomas.
CC -!- PTM: Has a high content of sialic acid and O-linked carbohydrate
CC structures.
CC -----
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CC -----
CC EMBL; X17018; CAA34884.1; -
CC EMBL; X52609; CAA36840.1; -
CC EMBL; S70677; AAB30765.1; -
CC EMBL; M30693; AAA39457.1; -
CC -----

DR PIR; A43545; A43545.
DR MGD; MGI:98384; Spt.
KW Glycoprotein; Transmembrane; Signal; T-cell; Antigen.
FT SIGNAL 1 19
FT CHAIN 20 395 LEUKOSIALIN
FT DOMAIN 20 248 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 249 271 POTENTIAL.
FT DOMAIN 272 395 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 167 167 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 395 AA; 40038 MW; 369F201B04DBC055 CRC64;

Query Match 10.6%; Score 96; DB 1; Length 395;
Best Local Similarity 33.7%; Pred. No. 0.4; Mismatches 36; Indels 10; Gaps 4;
Matches 31; Conservative 15;

QY 46 TGHSTSLFPTALQP-QEGSALRPDVALLVGAPALLGLILATLVGLVSLVSWNRQQLR 104
DB 228 TSTSTQDPTITRSPQSSGM-----LLV-PMILALVWLALVAL--LLLWRQQRKR 278

QY 105 TASPDTSEGVQGESLENVFPSETPHASAPT 136
DB 279 TGAITLGGGKRGVVDWAGPARVPDEATT 310

RESULT 6
DDRL RAT
ID DDRL RAT STANDARD; PRT; 910 AA.
AC Q63474;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Epithelial discoidin domain receptor 1 precursor (EC 2.7.1.112)
DE (Tyrosine-protein kinase CAK) (Cell adhesion kinase) (Tyrosine kinase
DE DDR) (Discoidin receptor tyrosine kinase) (Protein-tyrosine kinase
DE PTK-3).
DE DDRL OR EDDR1 OR PTK3.
GN Rattus norvegicus (Rat).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Sprague-Dawley; TISSUE=Brain;
RX MEDLINE=94173920; PubMed=8127887;
RA Sanchez M.P., Tapley P., Saini S.S., He B., Pulido D., Barbacid M.;
RT "Multiple tyrosine protein kinases in rat hippocampal neurons:
RT isolation of Ptk-3, a receptor expressed in proliferative zones of
RL the developing brain.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:1819-1823(1994).
CC -!- FUNCTION: MAY BE INVOLVED IN CELL-CELL INTERACTIONS AND
CC RECOGNITION (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: VARIOUS EMBRYONIC AND ADULT TISSUES; ALSO
CC PROLIFERATIVE ZONES OF THE DEVELOPING BRAIN; HIPPOCAMPAL NEURONS.
CC -!- SIMILARITY: WITH THE CONSERVED CATALYTIC DOMAINS OF TYR-PROTEIN
CC KINASES.
CC -!- SIMILARITY: Contains 1 F5/8 type C domain.
CC -!- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. INSULIN
CC RECEPTOR SUBFAMILY.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@sb-sib.ch).
CC -----
CC EMBL; L26525; AAA21089.1; -
CC PIR; A53137; A53137.
CC HSSP; P00523; 2PTK.
CC -----
CC DR


```
FT DOMAIN 442 911 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 32 186 F5/8 TYPE C.
FT DOMAIN 379 413 GLY/PRO-RICH.
FT DOMAIN 474 599 GLY/PRO-RICH.
FT DOMAIN 608 903 PROTEIN KINASE.
FT NP BIND 614 622 ATP (BY SIMILARITY).
FT BINDING 653 653 ATP (BY SIMILARITY).
FT ACT SITE 764 764 BY SIMILARITY.
FT DISULFID 32 186 BY SIMILARITY.
FT MOD RES 511 511 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT MOD RES 790 790 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT MOD RES 794 794 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT MOD RES 795 795 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 213 213 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 372 372 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. .) (POTENTIAL).
FT VARSPLIC 503 539 Missing (in isoform CAK II).
FT FTIdaVSP 002954.
SQ SEQUENCE 911 AA; 101160 MW; DB7FE03DD79510 CRC64;

Query Match 9.6%; Score 87.5; DB 1; Length 911;
Best Local Similarity 30.2%; Pred. No. 5.4;
Matches 39; Conservative 19; Mismatches 38; Indels 33; Gaps 10;

Qy 44 PDTGHTSSLEPGTALQPO-----EGSALRPDVALVYCAPALLGLILALTGLVLSIV 95
Db 388 PPTNFNSLE-----LEPRGQOPVAKAGS-----PTAILIG-CLVAIIILLLLI--IALM 435

Qy 96 SWR--WRQQLRTASPTSEGVQOESLENVFPVS-----SETHASAPTWPPLKEDADSAL 148
Db 436 LWRLHWRLLSKAB--RRVLEBELTVHLSVPGDTILINRPGPREP--PPVQEPFRPGT 490

Qy 149 PRHSVP-VP 156
Db 491 PPHSAPCV 499

RESULT 8
LRBA_HUMAN
ID LRBA_HUMAN STANDARD; PRT; 2863 AA.
AC P50851; Q9H2U3; Q9H2U4;
DT 01-OCT-1996 (Rel. 34, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Lipopolysaccharide-responsive and beige-like anchor protein (CDCA4-like protein) (Beige-like protein).
DE LRBA OR LBA OR CDC4L OR BGL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21154060; PubMed=11254716;
RA Wang J.-W., Howson J., Haller E., Kerr W.G.;
RT "Identification of a novel lipopolysaccharide-inducible gene with key features of both A kinase anchor proteins and chsl/beige proteins.";
RL J. Immunol. 166:4586-4595(2001).
RN [2]
RP SEQUENCE OF 775-2692 FROM N.A.
RX MEDLINE=21154060; PubMed=11254716;
RA Mager D.L.;
RT Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 2179-2692 FROM N.A.
RX MEDLINE=92372019; PubMed=1505956;
RA Feuchter A.E., Freeman J.D., Mager D.L.;
RT "Strategy for detecting cellular transcripts promoted by human endogenous long terminal repeats: identification of a novel gene (CDC4L) with homology to yeast CDC4.";
RT Genomics 13:1237-1246(1992).
CC -!- SIMILARITY: Contains 6 WD repeats.
CC -!- INDUCTION: By lipopolysaccharide (LPS).
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CC -!- SIMILARITY: Contains 1 BEACH domain.
CC -!- CAUTION: WAS ORIGINALLY (REF.3) SAID TO BE SIMILAR TO YEAST CDC4, BUT THAT SIMILARITY IS VERY LIMITED.
CC -----
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CC -----
DR EMBL; AF216848; AAG48558.2; -.
DR EMBL; AF217149; AAG48559.1; -.
DR EMBL; M83822; AAB09603.1; -.
DR Genew; HGNC:1742; LRBA.
DR MIM; 606453; -.
DR InterPro; IPR000409; Beige_BEACH.
DR InterPro; IPR001680; WD40.
DR Pfam; PF021138; Beach; 1.
DR Pfam; PF00400; WD40; 5.
DR ProDom; PD007848; Beige_BEACH; 1.
DR SMART; SM00320; WD40; 5.
DR PROSITE; PS0197; BEACH; 1.
DR PROSITE; PS00678; WD_REPEATS_1; FALSE_NEG.
DR PROSITE; PS00882; WD_REPEATS_2; FALSE_NEG.
DR PROSITE; PS02394; WD_REPEATS_REGION; FALSE_NEG.
KW Repeat; WD repeat.
FT REPEAT 1301 1343 WD 1.
FT DOMAIN 2200 2489 BEACH.
FT REPEAT 2591 2633 WD 2.
FT REPEAT 2636 2679 WD 3.
FT REPEAT 2695 2735 WD 4.
FT REPEAT 2777 2816 WD 5.
FT REPEAT 2819 2856 WD 6.
FT CONFLICT 2674 2692 KCGI:GDNPGRSTAAPRAI -> NAVGLEITQAVRLILGP F (IN REF. 2 AND 3).
SQ SEQUENCE 2863 AA; 319157 MW; D58BE93A6E924C30 CRC64;

Query Match 9.6%; Score 87.5; DB 1; Length 2863;
Best Local Similarity 25.2%; Pred. No. 19;
Matches 51; Conservative 29; Mismatches 85; Indels 37; Gaps 8;

Qy 8 VRSQRSDS-SVPTQCNQTECFDPLVRNCVSCELPHTPTDGTHTSLEPGTALQPOEGSAL 66
Db 1428 IEAEKSMSSGGILRQCLRLVC-AVAVRNCLEQCHSOLKTRGDKALKPMHSLIPLGKSA 1486
Qy 67 RPDVALLVCA-----PALLGLILALTGLVLS-LVSW 97
Db 1487 KSPVDIVTGGISFVRDLRLQDMINRLRAVFRDIEDSKQAOFLALAVYFISVLMSV 1546
Qy 98 RWRQQLRTASPTSEGVQOESLENVFPVSSE-TPHA-SAPTWPPLKE-DADSALPRHSVP 154
Db 1547 KYRDIILEPQNERHSQSCITGSENVNLSLSEITPAAFSTLTITASVESESTSSARRRDSG 1606
Qy 155 V----PATELGSTELVTYTKAGP 173
Db 1607 IGEETATGLGSHVEVTPHTAPP 1628

RESULT 9
DDR1_HUMAN
ID DDR1_HUMAN STANDARD; PRT; 913 AA.
AC Q08345; Q14196; Q16562;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Epithelial discoidin domain receptor 1 precursor (EC 2.7.1.112)
DE (Tyrosine-protein kinase CAX) (Cell adhesion kinase) (Tyrosine kinase DDR) (Discoidin receptor tyrosine kinase) (TRK E) (Protein-tyrosine kinase RTK 6) (CD167a antigen).
DE DDR1 OR EDDR1 OR CAK OR TRKE OR RTK6.
OS Homo sapiens (Human).
```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal liver;
RX MEDLINE=9413417; PubMed=302582;
RA Perez J.L., Shen X., Finkernagel S., Sciorra L., Jenkins N.A.,
RA Gilbert D.J., Copeland N.G., Wong T.W.;
RT "Identification and chromosomal mapping of a receptor tyrosine kinase
RT with a putative phospholipid binding sequence in its ectodomain";
RL Oncogene 9:211-219(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=93296201; PubMed=8390675;
RA Johnson J.D., Edman J.C., Rutter W.J.;
RT "A receptor tyrosine kinase found in breast carcinoma cells has an
RT extracellular discoidin I-like domain";
RL Proc. Natl. Acad. Sci. U.S.A. 90:5677-5681(1993).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=97131588; PubMed=8977099;
RA Sakuma S., Tada M., Sawa H., Sawamura Y., Shinohara Y., Abe H.;
RT "Receptor protein tyrosine kinase DDR is up-regulated by p53
RT protein";
RL FEBS Lett. 398:165-169(1996).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=96399017; PubMed=8796349;
RA Playford M.P., Butler R.J., Wang X.C., Katso R.M., Cooke I.E.,
RA Ganesan T.S.;
RT "The genomic structure of discoidin receptor tyrosine kinase";
RL Genome Res. 6:620-627(1996).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM SHORT).
RC TISSUE=Lung;
RX MEDLINE=96204002; PubMed=8622863;
RA Perez J.L., Jing S.Q., Wong T.W.;
RT "Identification of two isoforms of the Cak receptor kinase that are
RT coexpressed in breast tumor cell lines";
RL Oncogene 12:1469-1477(1996).
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM SHORT).
RC TISSUE=Brain, and Keratinocytes;
RX MEDLINE=94043265; PubMed=8226977;
RA di Marco E., Cutuli N., Guerra L., Cancedda R., de Luca M.;
RT "Molecular cloning of trke, a novel trk-related putative tyrosine
RT kinase receptor isolated from normal human keratinocytes and widely
RT expressed by normal human tissues";
RL J. Biol. Chem. 268:24290-24295(1993).
RN [7]
RP SEQUENCE FROM N.A. (ISOFORM SHORT).
RC TISSUE=Ovary;
RX MEDLINE=95151638; PubMed=7848919;
RA Laval S., Butler R., Shelling A.N., Hanby A.M., Poulson R.,
RA Ganesan T.S.;
RT "Isolation and characterization of an epithelial-specific receptor
RT tyrosine kinase from an ovarian cancer cell line";
RL Cell Growth Differ. 5:1173-1183(1994).
RN [8]
RP SEQUENCE FROM N.A.
RA Shina S., Tamiya G., Oka A., Inoko H.;
RT "Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [9]
RP SEQUENCE FROM N.A. (ISOFORM SHORT).
RC TISSUE=Muscle;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan B., Moore S.I., Wang J., Heide F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Sapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalios D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: MAY BE INVOLVED IN CELL-CELL INTERACTIONS AND
CC RECOGNITION.
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=CAK I;
CC IsoId=Q08345-1; Sequence=Displayed;
CC Name=2; Synonyms=CAK II;
CC IsoId=Q08345-2; Sequence=VSP 002953;
CC -!- TISSUE SPECIFICITY: EXPRESSED AT LOW LEVELS IN MOST ADULT TISSUES
CC AND IS HIGHEST IN THE BRAIN AND LUNG. ABUNDANT IN BREAST CARCINOMA
CC CELL LINES.
CC -!- DOMAIN: THE GLY/PRO-RICH DOMAINS MAY BE REQUIRED FOR AN UNUSUAL
CC GEOMETRY OF INTERACTION WITH LIGAND OR SUBSTRATES.
CC -!- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. INSULIN
CC RECEPTOR SUBFAMILY.
CC -!- SIMILARITY: Contains 1 F5/8 type C domain.
CC -!- DATABASE: NAME=PROW; NOTE=PROW 1:41-46(2000);
CC WWW="http://www.ncbi.nlm.nih.gov/prov/guide/1986613159_g.htm".
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L11315; AAA02866.1; -;
DR EMBL; L20817; AAA18019.1; -;
DR EMBL; U48705; AAC50917.1; -;
DR EMBL; X98208; CAA66871.1; -;
DR EMBL; X99023; CAA66871.1; JOINED.
DR EMBL; X99024; CAA66871.1; JOINED.
DR EMBL; X99025; CAA66871.1; JOINED.
DR EMBL; X99026; CAA66871.1; JOINED.
DR EMBL; X99027; CAA66871.1; JOINED.
DR EMBL; X99028; CAA66871.1; JOINED.
DR EMBL; X99029; CAA66871.1; JOINED.
DR EMBL; X99030; CAA66871.1; JOINED.
DR EMBL; X99031; CAA66871.1; JOINED.
DR EMBL; X99032; CAA66871.1; JOINED.
DR EMBL; X99033; CAA66871.1; JOINED.
DR EMBL; X99034; CAA66871.1; JOINED.
DR EMBL; L57508; AAB05208.1; -;
DR EMBL; X74979; CAA52915.1; -;
DR EMBL; Z29093; CAA82335.1; -;
DR EMBL; AP000511; BAB63318.1; -;
DR EMBL; BC008716; AAH08716.1; -;
DR EMBL; BC013400; AAH13400.1; -;
DR PIR; A48280; A48280.
DR PIR; A49508; A49508.
DR HSSP; P11362; 1FGK.
DR Genew; HGNC:2730; DDR1.
DR MIM; 600408; -;

DR GO: 0005987; C: integral to plasma membrane; TAS.
DR GO: 0004714; F: transmembrane receptor protein tyrosine kin. . .; TAS.
DR GO: 0007155; P: cell adhesion; TAS.
DR InterPro: IPR000431; FA5C.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002011; RTK_inaseII.
DR InterPro: IPR001245; Tyr_kinase.
DR Pfam: PF00754; F5_F8_type_C; 1.
DR Pfam: PF00669; pkinase; 1.
DR PRINTS: PR00109; TYRKINASE.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00231; FA58C; 1.
DR SMART: SM00219; Tyrc; 1.
DR PROSITE: PS01285; FA56C; 1; 1.
DR PROSITE: PS01286; FA58C; 2; 1.
DR PROSITE: PS00022; FA58C; 3; 1.
DR PROSITE: PS00107; PROTEIN KINASE ATP; FALSE_NEG.
DR PROSITE: PS00011; PROTEIN KINASE DOM; 1.
DR PROSITE: PS00109; PROTEIN KINASE TYR; 1.
DR PROSITE: PS00239; RECEPTOR TYR_KIN II; 1.
DR Transferase: Tyrosine-protein kinase; Glycoprotein; Signal;
KW phosphorylation; Transmembrane; Receptor; ATP-binding; Antigen;
KW Alternative splicing.
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 913 EPIITHELIAL DISCOIDIN DOMAIN RECEPTOR 1.
FT DOMAIN 19 416 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 417 443 POTENTIAL.
FT DOMAIN 444 913 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 31 185 F5/F8 TYPE C.
FT DOMAIN 377 415 GLY/PRO-RICH.
FT DOMAIN 476 601 GLY/PRO-RICH.
FT DOMAIN 610 905 PROTEIN KINASE.
FT NP_BIND 616 624 ATP (BY SIMILARITY).
FT BINDING 655 655 ATP (BY SIMILARITY).
FT ACT_SITE 766 766 BY SIMILARITY.
FT DISULFID 31 185 BY SIMILARITY.
FT MOD_RES 513 513 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT MOD_RES 792 792 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT MOD_RES 796 796 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT MOD_RES 797 797 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT CARBOHYD 211 211 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 260 260 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 371 371 N-LINKED (GLCNAC. .) (POTENTIAL).
Query Match 9.4%; Score 85.5; DB 1; Length 913;
Best Local Similarity 30.2%; Pred. No. 8.1;
Matches 39; Conservative 19; Mismatches 38; Indels 33; Gaps 10;
Qy 44 PDTGHTSLPGTALQPO-----EGSALRPDVALVGPALLGLILALTGLVGLV 95
Db 390 PPTNFSSLE---LEPRGQPVAKEGS---PRLIG--CLVAIIILLILI--IALM 437
Qy 96 SWR--WRCQLRTASPTSGVQGESLENVFPVS-----SETHASAPTWPPPKEDADSAL 148
Db 438 LWRLHWRLLSKAE---RRVLEBELAVHLSVPGDTILNNRPGPREP--PPYQEPFRPRGN 492
Qy 149 PRHSVP-VP 156
Db 493 PPHSAPCV 501
RESULT 10
LEUK_RAT
ID LEUK_RAT STANDARD; PRT; 378 AA.
AC P13838;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Leukosialin precursor (Leucocyte sialoglycoprotein) (Sialophorin)
DE (CD43) (W3/13 antigen) (Fragment).
GN SPN.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Thymocytes;
RX MEDLINE=88166646; PubMed=2965006;
RA Killeen N., Barclay A.N., Willis A.C., Williams A.F.;
RT "The sequence of rat leukosialin (W3/13 antigen) reveals a molecule with O-linked glycosylation of one third of its extracellular amino acids";
RL EMBL J. 6:4029-4034 (1987).
RN [2]
RP BINDING TO SN.
RX MEDLINE=21136329; PubMed=11238599;
RA van den Berg T.K., Nath D., Ziltener H.J., Vestweber D., Fukuda M.,
RA van Die I., Crocker P.R.;
RT "CD43 functions as a T cell counterreceptor for the macrophage adhesion receptor sialoadhesin (Siglec-1)";
RL J. Immunol. 166:3637-3640 (2001).
CC -I- FUNCTION: One of the major glycoproteins of thymocytes and T lymphocytes. Plays a role in the physicochemical properties of the T-cell surface and in lectin binding. Presents carbohydrate ligands to selectins. Has an extended rodlike structure that could protrude above the glycocalyx of the cell and allow multiple glycan chains to be accessible for binding. Is a counterreceptor for SN/Siglec-1. During T-cell activation is actively removed from the T-cell-APC (antigen-presenting cell) contact site thus suggesting a negative regulatory role in adaptive immune response (By similarity).
CC -I- SUBCELLULAR LOCATION: Type I membrane protein.
CC -I- TISSUE SPECIFICITY: Cell surface of thymocytes, T lymphocytes, neutrophils, plasma cells and myelomas.
CC -I- PTM: Has a high content of sialic acid and O-linked carbohydrate structures.
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CC EMBL: Y00030; CAA68281.1; --.
DR PIR: S00842; S00842.
KW Glycoprotein; Transmembrane; Signal; T-cell; Antigen.
FT NON_TER 1 1
FT SIGNAL <1 7
FT CHAIN 8 378 LEUKOSIALIN.
FT DOMAIN 8 231 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 232 254 POTENTIAL.
FT DOMAIN 235 378 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 13 13 O-LINKED (GALNAC. .).
FT CARBOHYD 15 15 O-LINKED (GALNAC. .).
FT CARBOHYD 20 20 O-LINKED (GALNAC. .).
FT CARBOHYD 23 23 O-LINKED (GALNAC. .).
FT CARBOHYD 25 25 O-LINKED (GALNAC. .).
FT CARBOHYD 27 27 O-LINKED (GALNAC. .).
FT CARBOHYD 28 28 O-LINKED (GALNAC. .).
FT CARBOHYD 29 29 O-LINKED (GALNAC. .).
FT CARBOHYD 33 33 O-LINKED (GALNAC. .).
FT CARBOHYD 34 34 O-LINKED (GALNAC. .).
FT CARBOHYD 36 36 O-LINKED (GALNAC. .).
FT CARBOHYD 37 37 O-LINKED (GALNAC. .).
FT CARBOHYD 40 40 O-LINKED (GALNAC. .).
FT CARBOHYD 108 108 O-LINKED (GALNAC. .).
FT CARBOHYD 113 113 O-LINKED (GALNAC. .).
FT CARBOHYD 118 118 O-LINKED (GALNAC. .).
FT CARBOHYD 120 120 O-LINKED (GALNAC. .).
FT CARBOHYD 124 124 O-LINKED (GALNAC. .).
FT CARBOHYD 125 125 O-LINKED (GALNAC. .).
FT CARBOHYD 126 126 O-LINKED (GALNAC. .).
FT CARBOHYD 174 174 O-LINKED (GALNAC. .).
(POTENTIAL).

FT CARBOHYD 176 176 O-LINKED (GALNAC. . .)
FT CARBOHYD 180 180 O-LINKED (GALNAC. . .)
FT CARBOHYD 183 183 O-LINKED (GALNAC. . .) (POTENTIAL).
FT CARBOHYD 187 187 O-LINKED (GALNAC. . .)
FT CARBOHYD 189 189 O-LINKED (GALNAC. . .)
SQ SEQUENCE 378 AA; 38425 MW; 231CC808BA8A257C CRC64;

Query Match 9.4%; Score 85; DB 1; Length 378;
Best Local Similarity 24.1%; Pred. No. 3.4;
Matches 48; Conservative 19; Mismatches 74; Indels 58; Gaps 7;

QY 14 RDSVVP--TQCNECPDPLVRNCVSCLEFHTPTDGTGHTSLEPG----- 55
DB 137 KGTSAAPPVTVTSMTSGFPVATVTSSETSGPPVTWATGSLGSKETHGLSATIATSSGE 196
QY 56 -----TALQOEGSALRPDVALVIGAPALGLILATLVL 91
DB 197 SSSVAGTTPVFTKISTTSTPNPTTTPPPGSS---GMLLVLS--MLIALTVLVLVAL 250
QY 92 VSLVSWRWRQQLRTASPDTSBGVQESLENVFPSSGETPHASAPTWPPLKEDADSALPRH 151
DB 251 --LLLRQKQKERTGALTSLRGKRGKGTVDAMAGPARVPDEEATT-----ASGSGGNK 301
QY 152 SVFVPATLSTGLTVTKT 170
DB 302 SSGAPETD-GSGQPTLT 319

RESULT 11
ID ADRM MOUSE STANDARD; PRT; 407 AA.

AC Q9JKV1;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Adhesion regulating molecule 1 precursor (110 kDa cell membrane glycoprotein) (Gp110) (ARM-1).
GN ADRM1 OR Gp110.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1] _
RN SEQUENCE FROM N.A.
RX MEDLINE=20374361; PubMed=10919708;
RA Simms A.B., Weighardt H., Weidner K.M., Weidle U.H., Holzmann B.; "Functional cloning of ARM-1, an adhesion-regulating molecule upregulated in metastatic tumor cells.";
RL Clin. Exp. Metastasis 17:641-648(1999).
CC 1- FUNCTION: Promotes cell adhesion.
CC 1- SIMILARITY: BELONGS TO THE GP110 FAMILY.
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CC -----
DR EMBL; AF225959; AAF33401.1; -
DR MGD; MGI:1929289; Adrm1.
DR InterPro; IPR006773; ARM 1.
DR Pfam; PF04683; ARM 1; 1.
KW Cell adhesion; Glycoprotein; Signal.
FT SIGNAL 1 17
FT CHAIN 18 407
FT DOMAIN 135 202
FT DOMAIN 193 257
FT DOMAIN 203 213
FT POLY-SER.
FT CARBOHYD 162 162 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 250 250 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 407 AA; 42026 MW; 2A6C2691E79C962D CRC64;

Query Match 9.2%; Score 83; DB 1; Length 407;
Best Local Similarity 26.1%; Pred. No. 5.5;
Matches 47; Conservative 21; Mismatches 86; Indels 26; Gaps 8;

QY 2 GABRLVRQRSDSVPTQCNO--TECFD--PLVRNCVSCLEFHTPTDGTGHT--TSSLPEGTA 57
DB 101 GSKLEFFWQEPKTDDEBCHKNECLNNPMPGS-----LGASGSGSHLSALGGEGG 155
QY 58 LQOEGSALRPDVALVIGAPAL--LGLILATLVLGLVSLVSWRWRQQLRTASPDTSBGVQ 115
DB 156 LQSLGNMHSOLMQLIGPAGLGGGLGALTGPGLASLLG-----SSGPPASSSSSS 208
QY 116 QESLENVFPSSGETPHASAPTWPPLKEDADSALPRHSPVDPATELGSTELVTTKTAGPEQ 175
DB 209 SRQSAVTFSSSTTSARATPAPAPASATSPS---PAPSSGNG-----TSTAASPTQ 260

RESULT 12
ID ALC1 HUMAN STANDARD; PRT; 353 AA.

AC P01876;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig alpha-1 chain C region.
GN IGHAI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1] _
RN SEQUENCE FROM N.A.
RX MEDLINE=84130179; PubMed=6421489;
RA Planagan J.G., Lefranc M.-P., Rabbitts T.H.; "Mechanisms of divergence and convergence of the human immunoglobulin alpha 1 and alpha 2 constant region gene sequences.";
RL Cell 36:681-688(1984).
[2] _
RN SEQUENCE (MYELOMA PROTEIN BUR), AND DISULFIDE BONDS.
RX MEDLINE=79151016; PubMed=107164;
RA Putnam F.W., Liu Y.-S.V., Low T.L.K.; "Primary structure of a human IgA1 immunoglobulin. IV. Streptococcal IgA1 protease, digestion, Fab and Fc fragments, and the complete amino acid sequence of the alpha 1 heavy chain.";
RL J. Biol. Chem. 254:2865-2874(1979).
[3] _
RN SEQUENCE (MYELOMA PROTEIN TRO).
RX MEDLINE=76023781; PubMed=809331;
RA Kratzin H., Altevoigt P., Ruban E., Kortt A., Staroscik K., Hilschmann N.; "The primary structure of a monoclonal IgA-immunoglobulin (IgA Tro.), II. The amino acid sequence of the H-chain, alpha-type, subgroup III; structure of the complete IgA-molecule.";
RL Hoppe-Seyler's Z. Physiol. Chem. 356:1337-1342(1975).
[4] _
RN DISULFIDE BONDS.
RX MEDLINE=80114124; PubMed=393607;
RA Yang C.-Y., Kratzin H., Gotz H., Hilschmann N.; "Rule of antibody structure. Primary structure of a human monoclonal IgA-immunoglobulin (myeloma protein Tro). VII. Purification and characterization of the disulfide bridges.";
RL Hoppe-Seyler's Z. Physiol. Chem. 360:1919-1940(1979).
[5] _
RN REVIEW.
RX MEDLINE=91054387; PubMed=2241915;
RA Kerr M.A.; "The structure and function of human IgA.";
RL Biochem. J. 271:285-296(1990).
CC 1- FUNCTION: IG ALPHA IS THE MAJOR IMMUNOGLOBULIN CLASS IN BODY SECRETIONS. IT MAY SERVE BOTH TO DEFEND AGAINST LOCAL INFECTION AND TO PREVENT ACCESS OF FOREIGN ANTIGENS TO THE GENERAL IMMUNOLOGIC SYSTEM.

Db	179	LCGCVSVSSVLP	PCGACRWHWGKTKFTCTAAYPEBSKPTLATILSKSGNTFRPVP	HLPP	PPSE	238
QY	159	ELGSTE	ELVT	167		
Db	239	ELALNELVT	247			
RESULT 13						
PKM2_COREF						
ID	PKM2_COREF	STANDARD;	PFT;	520	AA.	
AC	Q8FUI4;					
DT	15-SEP-2003	(Rel. 42, Created)				
DT	15-SEP-2003	(Rel. 42, Last sequence update)				
DT	15-SEP-2003	(Rel. 42, Last annotation update)				
DE	Serine/threonine protein kinases drp72	(EC 2.7.1.37).				
GN	CE0034.					
OS	Corynebacterium efficiens.					
OC	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;					
OC	Corynebacterineae; Corynebacteriaceae; Corynebacterium.					
OX	NCBI_TaxID=152794;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN:YS-314 / AJ 12310 / DSM 44549 / JCM 11189;					
RA	Kawarayashi Y., Yamazaki J., Hino Y., Kikuchi H., Nakamura Y.,					
RA	Ikeo K., Suzuki M., Mashima J., Itoh T., Yamagishi A., Nishio Y.,					
RA	Usuda Y., Sugimoto S.;					
RT	"The entire genomic sequence of Corynebacterium efficiens YS-314.";					
RL	Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.					
CC	-!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.					
CC	-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.					
CC	-----					
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/					
CC	or send an email to license@isb-sib.ch).					
CC	-----					
CC	EMBL; AP005214; BAC16844.1; ..					
DR	InterPro; IPR000719; Prot_kinase.					
DR	InterPro; IPR002290; Ser_Thr_kinase.					
DR	InterPro; IPR001245; Tyr_kinase.					
DR	Pfam; PF00069; pkinase; 1.					
DR	ProDom; PD000001; Prot_kinase; 1.					
DR	SMART; SM00220; S_TKc; 1.					
DR	SMART; SM00219; TyrKc; 1.					
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.					
DR	PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.					
DR	PROSITE; PS00108; PROTEIN_KINASE_ST; 1.					
DR	Transferrase; Serine/threonine-protein kinase; ATP-binding;					
KW	Complete proteome.					
KW	DOMAIN 20 281					
FT	DOMAIN 372 492					
FT	PRO/THR-RICH.					
FT	NE BIND 26 34					
FT	FT BIND 49 49					
FT	ATP (BY SIMILARITY).					
FT	ATP (BY SIMILARITY).					
FT	ACT SITE 148 148					
FT	BY SIMILARITY.					
SEQ	SEQUENCE 520 AA; 54630 MW; 84CC987FE9F902F9 CRC64;					
Query Match	9.1%; Score 82.5; DB 1; Length 520;					
Best Local Similarity	21.1%; Pred. No. 7.9; Indels 37; Gaps 6;					
Matches 35; Conservative	24; Mismatches					
QY	31	LVRENVCSELEFHTPDTCGTSLSLFGTALOPQE	-----	GSALRPDVALV	GCAPAL	79
Db	274	LARAVSAVRLGNRPFPQHPSPAVQ-ATAVAPSPSASTAMLGQVARPTTSVPASPTVLP	PERQ	332		
QY	80	-----	IGHLIALTLVGLSVLSWNRQQLTASPDTS	SEGVCQESLENVFP	-----	SS 127
Db	333	EKRGGVGLGLIIIAAVTAIVIGGIIWAGATGV--FSGDSEETTTTETITQIVTPI	TTTS	390		
QY	128	ETPHASAPTWPLKEDADSALPRHSVPVPATELGSLTELVTTKTAGP	173			

Db 391 BEPTLAPPPVQTRQ-----PVPTDETPTRLPTTQESP 425

RESULT 14

TR16 CHICK

ID TR16_CHICK STANDARD; PRT; 416 AA.

AC P18519;

DT 01-NOV-1990 (Rel. 16, Last sequence update)

DT 01-NOV-1990 (Rel. 16, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Tumor necrosis factor receptor superfamily member 16 precursor (Low-affinity nerve growth factor receptor) (NGF receptor) (Gp90-LNGFR)

DE (p75 ICD) (Low affinity neurotrophin receptor p75NTR).

DE NGFR OR TNFRSF16.

GN Gallus gallus (Chicken).

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauaria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

OX NCBI_TaxID=9031;

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RX MEDLINE=90166579; PubMed=2560385;

RA Large T.H., Weskamp G., Helder J.C., Radeke M.J., Misko T.P., Shooter E.M., Reichardt L.F.;

RA "Structure and developmental expression of the nerve growth factor receptor in the chicken central nervous system."

RT Receptor in the chicken central nervous system."

RL Neuron 2:1123-1134(1989).

RN [2]

RP SEQUENCE OF 21-416 FROM N.A.

RX MEDLINE=90152140; PubMed=2154393;

RA Heuer J.G., Patemie-Nainie S., Wheeler E.F., Bothwell M.;

RA "Structure and developmental expression of the chicken NGF receptor."

RL Dev. Biol. 137:287-304(1990).

CC -!- FUNCTION: Low affinity receptor which can bind to NGF, BDNF, NT-3, and NT-4. Can mediate cell survival as well as cell death of neural cells (By similarity).

CC -!- SUBUNIT: Homodimer; disulfide-linked. Interacts with p75NTR-associated cell death executor. Interacts with TRAF2, TRAF4 and TRAF6 (By similarity).

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- PTM: N- AND O-glycosylated.

CC -!- PTM: Phosphorylated on serine residues.

CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.

CC -!- SIMILARITY: Contains 1 death domain.

DR PIR; JN0006; JN0006.

DR HSP; P07174; INGR.

DR InterPro; IPR000488; Death.

DR InterPro; IPR001368; TNFR_c6.

DR Pfam; PF00531; Death; 1.

DR Pfam; PF00020; TNFR_c6; 4.

DR SMART; SM00005; DEATH; 1.

DR SMART; SM00208; TNFR; 3.

DR PROSITE; PS00652; TNFR_NGFR_1; 3.

DR PROSITE; PS00050; TNFR_NGFR_2; 3.

DR PROSITE; PS0017; DEATH_DOMAIN; 1.

KW Receptor; Apoptosis; Neurogenesis; Transmembrane; Glycoprotein; Repeat; Phosphorylation; Signal.

FT SIGNAL 1 19

FT CHAIN 20 416

FT TUMOR NECROSIS FACTOR RECEPTOR

FT SUPERFAMILY MEMBER 16.

FT EXTRACELLULAR (POTENTIAL).

FT POTENTIAL.

FT DOMAIN 29 239

FT TRANSMEM 240 261

FT DOMAIN 262 416

FT REPEAT 23 57

FT REPEAT 58 99

FT REPEAT 100 138

FT REPEAT 140 180

FT DOMAIN 333 410

FT DEATH.

FT DOMAIN 188 236

FT SER/THR-RICH.

FT BY SIMILARITY.

FT DISULFID 24 35

FT BY SIMILARITY.

FT DISULFID 39 56 BY SIMILARITY.

FT DISULFID 59 75 BY SIMILARITY.

FT DISULFID 78 91 BY SIMILARITY.

FT DISULFID 81 99 BY SIMILARITY.

FT DISULFID 101 114 BY SIMILARITY.

FT DISULFID 117 130 BY SIMILARITY.

FT DISULFID 120 138 BY SIMILARITY.

FT DISULFID 141 156 BY SIMILARITY.

FT DISULFID 159 172 BY SIMILARITY.

FT DISULFID 162 180 BY SIMILARITY.

FT CARBOHYD 52 52 N-LINKED (GLCNAC...) (POTENTIAL).

FT CONFLICT 36 36 C -> Y (IN REF. 2).

FT CONFLICT 173 173 T -> K (IN REF. 2).

FT CONFLICT 276 276 N -> S (IN REF. 2).

FT CONFLICT 396 396 K -> R (IN REF. 2).

SQ SEQUENCE 416 AA; 44654 MW; 6BCEAA54F4D2D56 CRC64;

Query Match 9.0%; Score 82; DB 1; Length 416;

Best Local Similarity 24.1%; Pred. No. 6.8;

Matches 54; Conservative 22; Mismatches 64; Indels 84; Gaps 13;

QY 15 DSSVP-TQCNQTECFDPLVNCVS-----CELFHPTDTHGHTSSLEPTALQP-----Q 61

Db 154 DPLCPCTICEENEV---MVKECTATSDAECRLHPRWTHHTPSLAGSDSPFITRDPNT 210

QY 62 EGSA--LRPDVALLVG-----APALLGL---ILALTILVGLVSLVSW-RW----- 99

Db 211 EGMATLADIVITVWGSSQPVVSRGTADNLIPVCSILAAVVVGLVAVIAFKRWNSCKQN 270

QY 100 -----RQQLRTASP-----DTSEGVQOESLENVFPSPSETP-----HASAP- 135

Db 271 KQGANRRPVNQTPSPGKLSHDSGISVDSQSLHQPPNQSTQGPAPKGDGSLYASLPP 330

QY 136 -----TWPPPL-----KEDADSALPRHSVPVPA 157

Db 331 SKQEEVEKLLSSAAETWRLQAGELGYKEDLDCTREESPARA 374

RESULT 15

ALC1 GORGO

ID ALC1_GORGO STANDARD; PRT; 353 AA.

AC P20758;

DT 01-FEB-1991 (Rel. 17, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Ig alpha-1 chain C region.

GN IGHA1.

OS Gorilla gorilla gorilla (Lowland gorilla).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.

OX NCBI_TaxID=9595;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Lymph node;

RX MEDLINE=89386006; PubMed=2506527;

RA Kawamura S., Omoto K., Ueda S.;

PT "Nucleotide sequence of the gorilla immunoglobulin alpha 1 gene."

RL Nucleic acids Res. 17:6732-6732(1989)

CC -!- FUNCTION: IG ALPHA IS THE MAJOR IMMUNOGLOBULIN CLASS IN BODY SECRETIONS. IT MAY SERVE BOTH TO DEFEND AGAINST LOCAL INFECTION AND TO PREVENT ACCESS OF FOREIGN ANTIGENS TO THE GENERAL IMMUNOLOGIC SYSTEM.

CC -!- SIMILARITY: Contains 3 immunoglobulin-like domains.

CC -----

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CC -----

CC EMBL; X15045; CAA33147.1; ALT_INIT.

DR HSP; P01810; 2PBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig ci.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; Ig; 2.
DR PROSITE; PS50835; Ig-Like; 3.
DR PROSITE; PS00290; Ig_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; Repeat.
FT NON TER 1 1
FT DOMAIN 6 98 IG-LIKE 1.
FT DOMAIN 125 220 IG-LIKE 2.
FT DOMAIN 228 330 IG-LIKE 3.
FT DISULFID 14 14 INTERCHAIN (WITH LIGHT CHAIN) (BY
SIMILARITY).
FT DISULFID 26 85 BY SIMILARITY.
FT DISULFID 77 101 BY SIMILARITY.
FT DISULFID 122 122 INTERCHAIN (WITH HEAVY CHAIN) (BY
SIMILARITY).
FT DISULFID 123 180 OR 123-182 (BY SIMILARITY).
FT DISULFID 147 204 BY SIMILARITY.
FT DISULFID 182 182 INTERCHAIN (WITH HEAVY CHAIN) (OR 180).
FT DISULFID 192 192 INTERCHAIN (WITH HEAVY CHAIN OF ANOTHER
SUBUNIT) (BY SIMILARITY).
FT DISULFID 250 313 BY SIMILARITY.
FT DISULFID 352 352 INTERCHAIN (WITH J CHAIN) (BY
SIMILARITY).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 340 340 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 353 AA; 37755 MW; 4820E8D802AC7514 CRC64;

Query Match 9.0%; Score 81.5; DB 1; Length 353;
Best Local Similarity 25.3%; Pred. No. 6.3;
Matches 44; Conservative 19; Mismatches 72; Indels 39; Gaps 8;

QY 22 CNOCTCDPLVRNCVSCLEFHTPDTHGHTSSLEPGTALQPOEGSALRPDVALLVGAPALLG 81
DB 85 CHVAHYTNPSQDVTVPCKVPSTPTPTSPST--PPTSPSP--CCHPLSL--HRLPALED 136

QY 82 LI-----LALTVLGL--VSLVSWRWQRQLRTASPDTSQVQESLENVFPSSSTPHAS 133
DB 137 LLLGSEANLTCTLTGLRDASGVFTWTP---SSGKSAVEGPPERDLGGCYSVSSVLPQCA 193

QY 134 AP-----TWPFLEKEDASALPR-----HSVPVPATELGSELVT 167
DB 194 EPNHKGKFTCTAAYPESKTPLTATLSKGNMFRPEVHLPPPSBELALNELVT 247

Search completed: February 5, 2004, 17:59:35
Job time : 11.222 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 5, 2004, 17:55:39 ; Search time 29.6528 Seconds
(without alignments)
1522.933 Million cell updates/sec

Title: US-10-045-574b-28
Perfect score: 907
Sequence: 1 MGARRLRVRSQRSDSSVPT.....PATELGSTELVTTKTAGPEQ 175

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues
Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_23:
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rviro:*
16: sp_bacteriaph:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	902	99.4	175	11 Q8R4W8	Q8R4W8 mus musculus
2	102	11.2	295	4 Q9H746	Q9H746 homo sapien
3	102	11.2	845	4 Q9HAU3	Q9HAU3 homo sapien
4	102	11.2	845	4 Q9HBB8	Q9HBB8 homo sapien
5	102	11.2	845	4 Q9HBB5	Q9HBB5 homo sapien
6	99	10.9	651	4 Q9NXI9	Q9NXI9 homo sapien
7	95.5	10.5	911	11 Q35407	Q35407 mus musculus
8	94	10.4	291	6 Q9MZU9	Q9MZU9 felis silve
9	94	10.4	1326	4 Q75136	Q75136 homo sapien
10	93	10.3	831	11 Q8VHF2	Q8VHF2 mus musculus
11	92.5	10.2	438	13 Q9DFV0	Q9DFV0 brachydanio
12	92.5	10.2	563	16 Q84328	Q84328 chlamydia t
13	90.5	10.0	497	4 Q8WY24	Q8WY24 homo sapien
14	90	9.9	831	11 Q8CEJ3	Q8CEJ3 mus musculus
15	87.5	9.6	2851	4 Q8NFQ0	Q8NFQ0 homo sapien
16	87	9.6	315	11 Q8BPH8	Q8BPH8 mus musculus

17	86.5	9.5	744	4 Q8NHD2	Q8NHD2 homo sapien
18	85.5	9.4	898	11 Q8K1S4	Q8K1S4 mus musculus
19	85	9.4	862	11 Q9JIK1	Q9JIK1 rattus norv
20	85	9.4	1032	5 P91365	P91365 caenorhabdi
21	85	9.4	2232	5 Q8IFX6	Q8IFX6 caenorhabdi
22	84.5	9.3	246	4 Q14762	Q14762 homo sapien
23	84.5	9.3	1092	5 Q22463	Q22463 caenorhabdi
24	84.5	9.3	3262	11 Q9EQJ5	Q9EQJ5 mus musculus
25	84	9.3	159	16 Q9RUC5	Q9RUC5 deinococcus
26	84	9.3	295	12 Q3DWH0	Q3DWH0 rat cytomeg
27	84	9.3	857	16 Q98IK2	Q98IK2 rhizobium l
28	83.5	9.2	651	4 Q9NX86	Q9NX86 homo sapien
29	83.5	9.2	669	11 Q9D8I9	Q9D8I9 mus musculu
30	83	9.2	367	16 Q8Y030	Q8Y030 ralsstonia s
31	83	9.2	407	11 Q922A7	Q922A7 mus musculus
32	83	9.2	535	4 Q15175	Q15175 homo sapien
33	83	9.2	585	5 Q9VZA9	Q9VZA9 drosophila
34	83	9.2	750	3 Q9HFZ4	Q9HFZ4 candida alb
35	83	9.2	2787	2 Q9S1A9	Q9S1A9 microcystis
36	82.5	9.1	384	4 Q9UP60	Q9UP60 homo sapien
37	82.5	9.1	493	4 Q8NCL6	Q8NCL6 homo sapien
38	82.5	9.1	494	4 Q96K68	Q96K68 homo sapien
39	82.5	9.1	496	4 Q96KX8	Q96KX8 homo sapien
40	82.5	9.1	520	16 Q8FUI4	Q8FUI4 corynebacte
41	82.5	9.1	772	13 Q92070	Q92070 gallus gall
42	82.5	9.1	2766	11 Q9QZ88	Q9QZ88 rattus norv
43	82	9.0	409	5 Q9U0Z7	Q9U0Z7 leishmania
44	82	9.0	468	12 Q8JKN0	Q8JKN0 heliothis z
45	82	9.0	614	17 Q8TU88	Q8TU88 methanosarc

ALIGNMENTS

RESULT 1

Q8R4W8
ID Q8R4W8 PRELIMINARY; PRT; 175 AA.
AC Q8R4W8;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE TRAF3 binding protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Mizuno K., Irie S., Sato T.-A.;
RT "Identification of novel TRAF3 binding protein, T3BP, which increases cellular F-actin content.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF350257; AAL83914.1; -.
SQ SEQUENCE 175 AA; 18846 MW; B64EFF4B52EE93B1 CRC64;

Query Match 99.4%; Score 902; DB 11; Length 175;
Best Local Similarity 99.4%; Pred. No. 3.3e-75;
Matches 174; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	MGARRLRVRSQRSDSSVPTQCQTECFDPLVRNCVSCELFHTPTDHTTSSLEPGTALQP	60
Db	1	MGARRLRVRSQRSDSSVPTQCQTECFDPLVRNCVSCELFHTPTDHTTSSLEPGTALQP	60
Qy	61	QESGALRPDVALLVGAPALLGLILALTLVGLVSLVSWRQQLRTASPDTEGVQCESLE	120
Db	61	QESGALRPDVALLVGAPALLGLILALTLVGLVSLVSWRQQLRTASPDTEGVQCESLE	120
Qy	121	NVFPVPSSETPHSAPTWPPPLKEDADALSALPRHSPVPVPADELSTELVTTKTAGPEQ	175
Db	121	NVFPVPSSETPHSAPTWPPPLKEDADALSALPRHSPVPVPADELSTELVTTKTAGPEQ	175

RESULT 2

```
Q9H746
ID Q9H746 PRELIMINARY; PRT; 295 AA.
AC Q9H746;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE Hypothetical protein FLJ21359.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Oktani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T.,
RA Tanaka T., Nakamura Y., Isegai T., Sugano S.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK025012; BAB15052.1; -.
DR InterPro; IPR002365; Pric_h_extensn.
DR PRINTS; PR01217; PRICEXTENS.
KW Hypothetical protein.
SQ SEQUENCE 295 AA; 29184 MW; D1F2B24701356A8F CRC64;

Query Match 11.2%; Score 102; DB 4; Length 295;
Best Local Similarity 28.1%; Pred. No. 0.2;
Matches 41; Conservative 18; Mismatches 67; Indels 20; Gaps 4;

QY 43 TPDGHTSSLEFGTALQPOEGSALRP-----DVALLVGAPALLGLILALT 87
DB 77 TPGGTAQTPEPGTS-QPMPLSKSTPSGGGSDKRFVSVDMAALGG---VLGALLLLA 132
QY 88 LVGLVSLVSWRWQRLRTASPDTSSEGVQESLENVFPSSSTPHASAPTWPLKEDADSA 147
DB 133 LLGLAVLVKHVYGRKCCSGKAPQPOGFDNQAFDPDKANWAPVPSPTHDPKPAEAP 192
QY 148 LPRHSVPV-PATELGSTELVTTKTAG 172
DB 193 MPAEPAPPGPASPGGAPPEPPAARAG 218

RESULT 3
Q9HAU3
ID Q9HAU3 PRELIMINARY; PRT; 845 AA.
AC Q9HAU3;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Mu-protocadherin.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Soleiman A., Krieger S., Haase A., Hantusch B.;
RT "Cloning and characterization of human mu-protocadherin.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF301909; AAG33495.1; -.
DR Genew; HGNC:7521; MUCDHL.
DR InterPro; IPR002126; Cadherin.
DR PRINTS; PR00205; CADHERIN.
DR SMART; SM00112; CA; 3.
DR PROSITE; PS00232; CADHERIN_1; 1.
DR PROSITE; PS00268; CADHERIN_2; 4.
SQ SEQUENCE 845 AA; 88171 MW; D12C11C1E3E11680 CRC64;

Query Match 11.2%; Score 102; DB 4; Length 845;
Best Local Similarity 28.1%; Pred. No. 0.65;
Matches 41; Conservative 18; Mismatches 67; Indels 20; Gaps 4;
```

```
QY 43 TPDGHTSSLEFGTALQPOEGSALRP-----DVALLVGAPALLGLILALT 87
DB 627 TPGGTAQTPEPGTS-QPMPLSKSTPSGGGSDKRFVSVDMAALGG---VLGALLLLA 682
QY 88 LVGLVSLVSWRWQRLRTASPDTSSEGVQESLENVFPSSSTPHASAPTWPLKEDADSA 147
DB 683 LLGLAVLVKHVYGRKCCSGKAPQPOGFDNQAFDPDKANWAPVPSPTHDPKPAEAP 742
QY 148 LPRHSVPV-PATELGSTELVTTKTAG 172
DB 743 MPAEPAPPGPASPGGAPPEPPAARAG 768

RESULT 4
Q9HBB8
ID Q9HBB8 PRELIMINARY; PRT; 845 AA.
AC Q9HBB8;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE MUCDHL-FL.
GN MUCDHL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20487546; PubMed=110311102;
RA Paris M.J., Williams B.R.G.;
RT "Characterization of a 500-Kb Contig spanning the Region between c-Ha-
RT Ras and MUC2 on Chromosome 11p15.5.";
RL Genomics 69:196-202(2000).
DR EMBL; AF258674; AAG16731.1; -.
DR InterPro; IPR002126; Cadherin.
DR SMART; SM00112; CA; 3.
DR PROSITE; PS00232; CADHERIN_1; 1.
DR PROSITE; PS00268; CADHERIN_2; 4.
SQ SEQUENCE 845 AA; 88097 MW; 6CDOE3985391F59F CRC64;

Query Match 11.2%; Score 102; DB 4; Length 845;
Best Local Similarity 28.1%; Pred. No. 0.65;
Matches 41; Conservative 18; Mismatches 67; Indels 20; Gaps 4;

QY 43 TPDGHTSSLEFGTALQPOEGSALRP-----DVALLVGAPALLGLILALT 87
DB 627 TPGGTAQTPEPGTS-QPMPLSKSTPSGGGSDKRFVSVDMAALGG---VLGALLLLA 682
QY 88 LVGLVSLVSWRWQRLRTASPDTSSEGVQESLENVFPSSSTPHASAPTWPLKEDADSA 147
DB 683 LLGLAVLVKHVYGRKCCSGKAPQPOGFDNQAFDPDKANWAPVPSPTHDPKPAEAP 742
QY 148 LPRHSVPV-PATELGSTELVTTKTAG 172
DB 743 MPAEPAPPGPASPGGAPPEPPAARAG 768

RESULT 5
Q9HBB5
ID Q9HBB5 PRELIMINARY; PRT; 845 AA.
AC Q9HBB5;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE MUCDHL-FL.
GN MUCDHL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Paris M.J., Williams B.R.G.;
```

RT "MUCDHL, a Novel cDNA with Mucin and Cadherin-Like Domains."
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF258676; AA016733.1; -
DR InterPro; IPR002126; Cadherin.
DR PRINTS; PRO0205; CADHERIN.
DR SMART; SM00112; CA; 3
DR PROSITE; PS00232; CADHERIN_1; 1.
DR PROSITE; PS0269; CADHERIN_2; 4.
SQ SEQUENCE 845 AA; 88156 MW; 10E654279CB305CE CRC64;

Query Match 11.2%; Score 102; DB 4; Length 845;
Best Local Similarity 28.1%; Pred. No. 0.65;
Matches 41; Conservative 18; Mismatches 67; Indels 20; Gaps 4;

QY 43 TPDTGHTSSLEPGTALQPGSGALRP-----DVALVGPALLGILALT 87
DB 627 TPGGGTAQTPEPGTS-QPMPLSKSTPSSGGPSDEKRFVSVDMAALGG---VIGALLLLA 682
QY 88 LVGLVSLVSWRWRLQRLTASPDTSSEGVQBSLENVFPVSSETPHASAPTWPLPKEDADSA 147
DB 683 LLGLAVLVKHVYGRLLKCCSGKAPEQPQGFQDNQALPDHKNWAPVPSPTHPKPAEAP 742

QY 148 LPRHSVPV-PATELGSTELVTTKAG 172
DB 743 MPAPPPGPGSPGGAPEPPAAARAG 768

RESULT 6
Q9NXI9 PRELIMINARY; PRT; 651 AA.
AC Q9NXI9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein FLJ20219.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon mucosa;
RA Watanabe K., Kumagai A., Itakura S., Yamazaki M., Tashiro H., Ota T.,
RA Suzuki Y., Oobayashi M., Nishi T., Shibahara T., Tanaka T.,
RA Nakamura Y., Isegaki T., Sugano S.;
RT "NEDO human cDNA sequencing project."
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK000226; BAA91021.1; -.
DR InterPro; IPR002126; Cadherin.
DR PROSITE; PS0268; CADHERIN_2; 2.
KW Hypothetical protein.
SQ SEQUENCE 651 AA; 67379 MW; AB6D4984FDG9175C CRC64;

Query Match 10.9%; Score 99; DB 4; Length 651;
Best Local Similarity 28.3%; Pred. No. 0.91;
Matches 39; Conservative 18; Mismatches 61; Indels 20; Gaps 4;

QY 43 TPDTGHTSSLEPGTALQPGSGALRP-----DVALVGPALLGILALT 87
DB 461 TPGGGTAQTPEPGTS-QPMPLSKSTPSSGGPSDEKRFVSVDMAALGG---VIGALLLLA 516
QY 88 LVGLVSLVSWRWRLQRLTASPDTSSEGVQBSLENVFPVSSETPHASAPTWPLPKEDADSA 147
DB 517 LLGLAVLVKHVYGRLLKCCSGKAPEQPQGFQDNQALPDHKNWAPVPSPTHPKPAEAP 576

QY 148 LPRHSVPV-PATELGST 164
DB 577 MPAPPPGPGSPGGAPE 594

RESULT 7
Q95407 PRELIMINARY; PRT; 911 AA.
ID Q95407

AC Q95407;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Receptor-like tyrosine kinase (EC 2.7.1.112) (Tyrosine-protein kinase receptor).
DE DRP1 OR NEP.
GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129;
RX MEDLINE=93390947; PubMed=8397369;
RA Zerlin M., Julius M.A., Goldfarb M.;
RT "NEP: a novel receptor-like tyrosine kinase expressed in proliferating neuroepithelia."
RL Oncogene 8:2731-2739(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129;
RA Zerlin M., Julius M.A., Goldfarb M.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.

CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN TYROSINE PHOSPHATE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. INSULIN RECEPTOR SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 1 FS/8 TYPE C DOMAIN.

DR EMBL; AF026259; AAB81866.1; -.
DR HSP; P00523; 2PTK.
DR MGD; MGI:199216; Ddr1.
DR InterPro; IPR000421; FAS8 C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002011; RTKinaseII.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00754; F5_F8_type_C; 1.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00231; FAS8C; 1.
DR SMART; SM00219; Tyrc; 1.
DR PROSITE; PS01285; FAS8C_1; 1.
DR PROSITE; PS01286; FAS8C_2; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00239; RECEPTOR_TYR_KIN_II; 1.
KW ATP-binding; Glycoprotein; Kinase; Phosphorylation; Receptor;
KW Transferase; Transmembrane; Tyrosine-protein kinase.
SQ SEQUENCE 911 AA; 101091 MW; D52EC50267D8014D CRC64;

Query Match 10.5%; Score 95.5; DB 11; Length 911;
Best Local Similarity 31.4%; Pred. No. 2.8;
Matches 38; Conservative 17; Mismatches 49; Indels 17; Gaps 7;

QY 44 PDGTGHTSSLEPGTALQPGSGALRPDVALVGPALLGILALTGLVSLVSWR--WRQ 101
DB 388 PPTTFSSLELEPRGQOPVKGAGSTALIG--CLVAIIILLI--IALMLLHWR 443
QY 102 QLRTASPDTSSEGVQBSLENVFPVS-----STPHASAPTWPLPKEDADSA LPRHSVP-V 155
DB 444 LLSKAD---SRVLEELTVHLSVPGTILNNRPGPREP--PPYQEPRTGTPPHSAFCV 498
QY 156 P 156
DB 499 P 499

RESULT 8
Q9MZU9 PRELIMINARY; PRT; 291 AA.
ID Q9MZU9
AC Q9MZU9;

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DT 01-OCT-2000 (TREMELrel. 15, Created)
DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)
DE Flt3 ligand.
OS Felis silvestris carus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20358731; PubMed=10902925;
RX Yang S. Sim G.K.;
RT "Molecular cloning of canine and feline flt3 ligand reveals high
RT degree of similarity to the human and mouse homologue but uniquely
RT long cytoplasmic domain.";
RL DNA Seq. 11:163-166(2000).
DR EMBL; AF155149; AAF87089.1; -.
DR HSSP; P49771; IETE.
DR InterPro; IPR004213; Flt3_lig.
DR Pfam; PF02947; flt3_lig.
DR SMART; SM00219; TYRK; 1.
SQ SEQUENCE 291 AA; 32459 MW; 8F85A10A5EA0DC6 CRC64;

Query Match 10.4%; Score 94; DB 6; Length 291;
Best Local Similarity 29.2%; Pred. No. 1;
Matches 42; Conservative 11; Mismatches 59; Indels 32; Gaps 7;

QY 33 RNCVSC-ELFHTPDGHTSSLEPGTALQPGSALRPDVALVGCAPALLGLL---ALTL 88
DB 148 RNFSGCLELQCFDS-----STLPFRSPRALEATAPAPQALLLLLLLFPVALL 199

QY 89 VGLVLSVW---RW-----RQLRTASP-----DTSEGVQOESLENVFPSSSTPHA 132
DB 200 MSAACWLHWRRRWTPVPRQKTLRPRNHLPEDEPGLSQLET---GSFLDHA 255

QY 133 SAPTWPLKEDADSLPRHSVVP 156
DB 256 APLTLPFGWRQRPPTAPDPPIP 279

RESULT 9
O75136 PRELIMINARY; PRT; 1326 AA.
AC O75136;
DT 01-NOV-1998 (TREMELrel. 08, Created)
DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)
DE KIAA0641 protein (Fragment).
GN KIAA0641.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=98403880; PubMed=9734811;
RX Ishikawa K., Nagase T., Suyama M., Miyajima N., Tanaka A., Kotani H.,
RA Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. X.
RT The complete sequences of 100 new cDNA clones from brain which can
RT code for large proteins in vitro.";
RL DNA Res. 5:169-176(1998).
DR EMBL; AB014541; BAA31616.2; -.
DR HSSP; P12931; IFMK.
DR Genew; HGNC121; AATK.
DR InterPro; IPR00719; Prot_kinase.
DR InterPro; IPR002230; Ser_thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TYRK; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
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DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW ATP-binding; Transferase.
FT NON_TER 1
SQ SEQUENCE 1326 AA; 139961 MW; 5E2917B6A1FC0158 CRC64;

Query Match 10.4%; Score 94; DB 4; Length 1326;
Best Local Similarity 26.5%; Pred. No. 5.9;
Matches 54; Conservative 23; Mismatches 79; Indels 48; Gaps 10;

QY 1 MGARRL---RVRSQRSDSVPTQCNQTECPDPLVRNCVSCLEFHTPDGHTSSLEPQT 56
DB 619 VGARRAQRQHWASNVSNANNSGRC--PESWDPVSAGC-HAEGCFSPKQTPRASPEPY 675

QY 57 ALQP-----QEGSALRPDVALVGCAPALLGLIILALTLVGLVLSVSWRWQ----- 101
DB 676 PGEPLGLQAASAQEGFC-----CPGLPHLCQAQGLAPACLVTPSWTETASGGDHPQA 730

QY 102 --QLRTASPDTS-----EGVQOESLENVFPSSSTPHASAPTWPPLKEDADSLPRHSV 153
DB 731 EPKLAEEAGTTGPRLPSPVSPSQEGAPLSEE---ASAP-----DAPDALPDSET 780

QY 154 PVPATELGSTELVTT---KTAGPE 174
DB 781 PATGGEVSAIKLASALNGSSSPE 804

RESULT 10
Q8VHF2 PRELIMINARY; PRT; 831 AA.
AC Q8VHF2;
DT 01-MAR-2002 (TREMELrel. 20, Created)
DT 01-MAR-2002 (TREMELrel. 20, Last sequence update)
DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)
DE Mu-protocadherin.
GN M10074H01R1K.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=BALB/c; TISSUE=Colon;
RA Soleiman A., Krieger S.;
RT "Cloning and characterization of mouse mu-protocadherin.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF462391; AAL67856.1; -.
DR MGD; MGI:1913290; 1810074H01R1k.
DR InterPro; IPR002126; Cadherin.
DR InterPro; IPR002965; F-rich_extensn.
DR InterPro; IPR001412; ERNA-synt_1.
DR Pfam; PF00028; cadherin; 1.
DR PRINTS; PR01217; PRICHEXTENS.
DR SMART; SM00112; CA; 2.
DR PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
DR PROSITE; PS00232; CADHERIN_1; 1.
DR PROSITE; PS02268; CADHERIN_2; 2.
KW Calcium; Calcium-binding; Cell adhesion; Glycoprotein.
SQ SEQUENCE 831 AA; 88208 MW; F0ABF867A37F558B CRC64;

Query Match 10.3%; Score 93; DB 11; Length 831;
Best Local Similarity 27.4%; Pred. No. 4.3;
Matches 46; Conservative 18; Mismatches 64; Indels 40; Gaps 8;

QY 43 TPDGHTSSLEPGTALQPGSALR-----PDVALVGCAPALLGLIILALTLVGLVSL 94
DB 605 TPFGTSCSTATGPISLPSTGAGEQDQGRFSDVWAVLG---VLGALLLALICLVIL 661

QY 95 VSWRWQRLRTASPDTSSEGVQOESLENV-FVPS-----SETPH-----ASAPTWP 139
DB 662 VHKYRHLRACCSKASE-PQPSGYDNLTLFLPHKAKWSPTPNRKEPSPKLAQPLRPP 720

QY 140 LKEDADSLPRHSVFPVPADEL-GSTELV-----TTKTAGPE 174
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DR ProDom; PD007848; Beige_BEACH; 1.
DR PROSITE; PS50197; BEACH; 1.
KW Repeat; WD repeat.
SQ SEQUENCE 2851 AA; 317650 MW; 5D1530AFDD66CD97 CRC64;

Query Match 9.6%; Score 87.5; DB 4; Length 2851;
Best Local Similarity 25.2%; Pred. No. 55;
Matches 51; Conservative 29; Mismatches 85; Indels 37; Gaps 8;

QY 8 VRSQRSDS-SVPTQCNTECFDPLVNCVSCLEFHTPTDHTSLEPQTALQPOEGSAL 66
AC Q8CEJ3; PRELIMINARY; PRT; 831 AA.
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE MU-PROTODACHERIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK027913; BAC25662.1; -. BAF320A033B143C4 CRC64;
SQ SEQUENCE 831 AA; 88227 MW; 88227 MW; BAF320A033B143C4 CRC64;

Search completed: February 5, 2004, 18:00:50
Job time : 31.6528 secs

QY 159 ELGSTELVT 167
Db 383 ELALNELVT 391

RESULT 14
Q8CEJ3
ID Q8CEJ3 PRELIMINARY; PRT; 831 AA.
AC Q8CEJ3;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE MU-PROTODACHERIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK027913; BAC25662.1; -. BAF320A033B143C4 CRC64;
SQ SEQUENCE 831 AA; 88227 MW; 88227 MW; BAF320A033B143C4 CRC64;

Query Match 9.9%; Score 90; DB 11; Length 831;
Best Local Similarity 27.9%; Pred. No. 8;
Matches 48; Conservative 19; Mismatches 61; Indels 44; Gaps 10;

QY 43 TPDGHTSLEPQ-----TALQP-----QEGSALR---PDVALLVGPALLGLIALTIVG 90
Db 601 TFSGSPQTPKFGTSQTATGPIGAGGQGGQFSTVDMAVLGG---VLGALLLIALIC 657
QY 91 LVSLVSWRQRLRTASPTSEGVQESLENV-FVPS-----SETPH-----ASAP 135
Db 658 LVILVHKYRHLACCSKASE-PQPSGYDNLTLFDPHKAKWSPTPNRKPSPKLAQPP 716
QY 136 TWPPKEDADSLPHSVVPVPADEL-GSTELV-----TTKTAGPE 174
Db 717 LRAPPSPMSSPTPPSPSTPPSPQKASGPKTVQAGDSFSAVRSILTKERRPE 768

RESULT 15
Q8NFQ0
ID Q8NFQ0 PRELIMINARY; PRT; 2851 AA.
AC Q8NFQ0;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Beige-like protein.
GN LRBA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A.
RX MEDLINE=22150859; PubMed=12160729;
RA Dymcmin V.G., Chaganti S.R., Dymcmin K., Palanisamy N., Murty V.V.V.S.,
RA Dalla-Favera R., Chaganti R.S.K.;
RT "BCL8 is a Novel, Evolutionarily Conserved Human Gene Family Encoding
RT Proteins with Presumptive Protein Kinase A Anchoring Function.";
RL Genomics 80:158-165(2002).
DR EMBL; AF467287; AAM53530.1; -.
DR InterPro; IPR000409; Beige_BEACH.
DR InterPro; IPR001680; WD40.
DR Pfam; PF02138; Beach; 1.
DR Pfam; PF00400; WD40; 4.

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OM protein - protein search, using sw model

Run on: February 5, 2004, 17:49:14 ; Search time 36.4583 Seconds
(without alignments)
761.888 Million cell updates/sec

Title: US-10-045-574B-28

Perfect score: 907

Sequence: 1 MGARRLRVRSQRDSVPT.....PATELGSTELVTTKTAGPEQ 175

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	907	100.0	175	23	ABBS1489
2	907	100.0	175	23	ABBS1489
3	907	100.0	175	24	ABP97722
4	902	99.4	175	23	ABP78398
5	447	49.3	185	23	AAE22266
6	437	48.2	185	23	AAE22267
7	432	47.6	185	23	AAE22269
8	431	47.5	185	23	AAE22268
9	426	47.0	185	23	AAE22270

10	423	46.6	185	23	AAE22271
11	417	46.0	185	23	AAE22242
12	415.5	45.8	266	23	AAE22243
13	410.5	45.3	184	23	ABBS1483
14	410.5	45.3	184	24	AAE35227
15	410.5	45.3	184	24	ABP97721
16	347	38.3	65	23	AAE22247
17	240	26.5	73	23	AAE22251
18	235	25.9	73	23	AAE22250
19	205	22.6	73	23	AAE22249
20	190	20.9	73	23	AAE22248
21	173	19.1	70	23	AAE22252
22	168	18.5	70	23	AAE22254
23	167	18.4	70	23	AAE22253
24	164	18.1	70	23	AAE22256
25	163	18.0	70	23	AAE22261
26	162	17.9	70	23	AAE22255
27	159	17.5	70	23	AAE22257
28	158	17.4	70	23	AAE22263
29	157	17.3	70	23	AAE22262
30	154	17.0	70	23	AAE22259
31	154	17.0	70	23	AAE22260
32	153	16.9	70	23	AAE22258
33	152	16.8	70	23	AAE22265
34	150.5	16.6	328	23	ABBS1493
35	149	16.4	70	23	AAE22264
36	144	15.9	320	23	AAE22245
37	143	15.8	70	23	AAE22246
38	116.5	12.8	181	23	AAE15484
39	116.5	12.8	184	21	AAE08843
40	116.5	12.8	184	21	AAE94001
41	116.5	12.8	184	22	AAE09241
42	116.5	12.8	184	22	AAE00506
43	116.5	12.8	184	22	AAE60698
44	116.5	12.8	184	22	AAE71979
45	116.5	12.8	184	23	AAE28961

ALIGNMENTS

RESULT 1

ABBS1489
ID ABBS1489 standard; Protein; 175 AA.

AC ABBS1489;

DT 02-SEP-2002 (first entry)

XX Mouse Ztnfr12 protein SEQ ID NO:13.

DE Human; Ztnfr12; tumour necrosis factor receptor; cytostatic; immunosuppressive; dermatological; antiinflammatory; antidiabetic; neuroprotective; antirheumatic; antiarthritic; antiasthmatic; nephrotropic; hypotensive; gene therapy; B lymphocyte; tumour; autoimmune disorder; systemic lupus erythematosus; myasthenia gravis; multiple sclerosis; insulin dependent diabetes mellitus; asthma; rheumatoid arthritis; bronchitis; emphysema; renal disease; lymphoma; glomerulonephritis; vasculitis; chronic lymphoid leukaemia; nephritis; pyelonephritis; renal neoplasm; multiple myeloma; amyloidosis; light chain neuropathy; hypertension; large vessel disease; graft-versus host disease; graft rejection; Crohn's disease.

XX Mus sp.

XX WO200238766-A2.

PD 16-MAY-2002.

XX 05-NOV-2001; 2001WO-US47018.

XX 07-NOV-2000; 2000US-246449P.

PR 20-DEC-2000; 2000US-257131P.

PR 28-JUN-2001; 2001US-301715P.
PR 29-AUG-2001; 2001US-315565P.
XX (ZYMO) ZYMOGENETICS INC.
PA Gross JA, Xu W, Henne RM, Grant FJ;
PI WPI; 2002-508212/54.
DR N-PSDB; AEN89431.
XX Novel isolated human tumor necrosis factor receptor polypeptide, termed
PT Ztnfr12, useful for treating autoimmune disorders, emphysema, end
PT stage renal failure or renal disease and lymphoma
XX Disclosure; Page 140; 154pp; English.
PS The present invention describes a human tumor necrosis factor receptor
CC designated Ztnfr12 (I). (I) has cytostatic, immunosuppressive,
CC dermatological, antiinflammatory, neuroprotective, antidiabetic,
CC antirheumatic, antiarthritic, antiaschematic, nephrotropic and hypotensive
CC activities, and can be used in gene therapy. (I) can be used for
CC inhibiting, in a mammal, the activity of a ligand that binds Ztnfr12
CC (e.g. ZTNF4), for treating disorders and diseases associated with B
CC lymphocytes, activated B lymphocytes or resting B lymphocytes, and for
CC inhibiting the proliferation of tumour cells. (I) is useful for treating
CC autoimmune disorders such as systemic lupus erythematosus, myasthenia
CC gravis, multiple sclerosis, insulin dependent diabetes mellitus, asthma,
CC rheumatoid arthritis, bronchitis, emphysema and end stage renal failure
CC or renal disease such as glomerulonephritis, vasculitis, chronic lymphoid
CC leukaemia, nephritis, and pyelonephritis, and for treating renal
CC neoplasms, multiple myelomas, lymphomas, light chain neuropathy, or
CC amyloidosis, hypertension, large vessel diseases, graft-versus host
CC disease, graft rejection and Crohn's disease. (I) is useful for
CC modulating the immune system, for regulating B cell responses and
CC development, for modulating development of other cells, antibody
CC production and cytokine production, and for modulating T and B cell
CC communication. The present sequence represents mouse Ztnfr12 which is
CC given in the exemplification of the present invention.
XX Sequence 175 AA;
SQ
Query Match 100.0%; Score 907; DB 23; Length 175;
Best Local Similarity 100.0%; Pred. No. 5,4e-87;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGARLRVRSQRSDSSVPTQCNTCECFDPLVRNCVSCSELFHTPDGTGHTSSLEPGTALQP 60
Db 1 MGARLRVRSQRSDSSVPTQCNTCECFDPLVRNCVSCSELFHTPDGTGHTSSLEPGTALQP 60
QY 61 QEGSALRPDVALLVGAPALLGLILATLVGLVSLVSWRWQRQLRTASPDTSSEGVQESLE 120
Db 61 QEGSALRPDVALLVGAPALLGLILATLVGLVSLVSWRWQRQLRTASPDTSSEGVQESLE 120
QY 121 NVFVPSSTPHASAPTWPLKEDADSALPRHSVPVPATELGSITELVTTKTAGEQ 175
Db 121 NVFVPSSTPHASAPTWPLKEDADSALPRHSVPVPATELGSITELVTTKTAGEQ 175
RESULT 2
AAE22244
ID AAE22244 standard; Protein; 175 AA.
XX AAE22244;
XX AAE22244;
DT 25-JUL-2002 (first entry)
XX Murine BAFF receptor (BAFF-R) protein.
XX Murine; BAFF receptor; BAFF-R; cytostatic; hypotensive; inflammation;
KW Tumour Necrosis Factor; autoimmune disease; immunosuppressive; cancer;
KW myasthenia gravis; hypertension; organ transplantation; drug screening;
KW HIV; human immunodeficiency virus; genetic disorder; cardiovascular; TNF;
KW renal; rheumatoid arthritis; systemic lupus erythematosus; amyloidosis;

KW haemolytic anaemia; Chagas' disease; Grave's disease; glomerulonephritis;
KW multiple myeloma; chromosomal mapping; tissue typing; drug screening.
XX Mus musculus.
XX Key Location/Qualifiers
FT Domain 70..97
FT /label= Transmembrane_domain
XX W0200224909-A2.
XX 28-MAR-2002.
XX 06-SEP-2001; 2001WO-US28006.
XX 18-SEP-2000; 2000US-233152P.
XX 21-SEP-2000; 2000US-234140P.
XX 13-FEB-2001; 2001US-268499P.
XX 14-AUG-2001; 2001US-312185P.
XX (BIOJ) BIOGEN INC.
XX Ambrose CW, Thompson JS;
XX WPI; 2002-362428/39.
XX N-PSDB; AAD35411.
XX New human BAFF receptor proteins and nucleic acids, useful for
XX treating, preventing or delaying e.g. autoimmune diseases, cancers,
XX inherited genetic disorders involving B-cells, cardiovascular
XX disorders, or renal disorders -
XX Example 4; Fig 4b; 164pp; English.
XX The invention relates to human BAFF receptor (BAFF-R) nucleic acids and
XX proteins. BAFF-R is a B-cell activating factor belonging to the Tumour
XX Necrosis Factor (TNF) family, which is associated with the expression of
XX B-cells and immunoglobulins. The BAFF-R proteins, DNA and antibodies are
XX useful for treating, preventing or delaying autoimmune diseases, cancer,
XX tumorigenic conditions or inherited genetic disorders involving B-cells,
XX hypertension, cardiovascular disorders, immunosuppressive diseases, renal
XX disorders, inflammation, organ transplantation and HIV. Autoimmune
XX diseases, which can be treated or prevented by BAFF-R, include systemic
XX lupus erythematosus, rheumatoid arthritis, myasthenia gravis, autoimmune
XX haemolytic anaemia, idiopathic thrombocytopenia purpura, Chagas' disease
XX Grave's disease, anti-phospholipid syndrome, Wegener's granulomatosis,
XX poly-arthritis nodosa and rapidly progressive glomerulonephritis. Plasma
XX cells disorders e.g., multiple myeloma, Waldenstrom's macroglobulinaemia,
XX heavy-chain disease, primary or immunocyte-associated amyloidosis, and
XX monoclonal gammopathy of undetermined significance. The nucleic acids,
XX protein, protein homologues, and antibodies may further be used in
XX screening assays, in detection assays (chromosomal mapping, tissue typing
XX or forensic biology), predictive medicine (e.g. diagnostic or prognostic
XX assays, monitoring clinical trials, or pharmacogenomic). The polypeptides
XX are further useful as immunogens to raise anti-BAFF-R antibodies, or in
XX screening drugs or compounds that modulate BAFF-R activity or expression.
XX The present sequence is murine BAFF-R protein.
SQ Sequence 175 AA;
Query Match 100.0%; Score 907; DB 23; Length 175;
Best Local Similarity 100.0%; Pred. No. 5,4e-87;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGARLRVRSQRSDSSVPTQCNTCECFDPLVRNCVSCSELFHTPDGTGHTSSLEPGTALQP 60
Db 1 MGARLRVRSQRSDSSVPTQCNTCECFDPLVRNCVSCSELFHTPDGTGHTSSLEPGTALQP 60
QY 61 QEGSALRPDVALLVGAPALLGLILATLVGLVSLVSWRWQRQLRTASPDTSSEGVQESLE 120
Db 61 QEGSALRPDVALLVGAPALLGLILATLVGLVSLVSWRWQRQLRTASPDTSSEGVQESLE 120
QY 121 NVFVPSSTPHASAPTWPLKEDADSALPRHSVPVPATELGSITELVTTKTAGEQ 175

Db 121 NVFVPSSETPHASAPTWPLKEDADSDALPHRSVVPVDPATELGSTELVTTKTAGEPQ 175
|||||
RESULT 3
ABP97722
ID ABP97722 standard; Protein; 175 AA.
XX AC ABP97722;
XX DT 28-MAY-2003 (first entry)
XX DE Amino acid sequence of murine BR3 receptor.
XX KW Human; TAC1; BR3; receptor; tumour necrosis factor ligand; TNF ligand;
KW TALL-1; April; systemic lupus erythematosus.
XX OS Mus sp.
XX PN WO2003014294-A2.
XX PD 20-FEB-2003.
XX PF 24-JUL-2002; 2002WO-US23487.
XX PR 03-AUG-2001; 2001US-310114P.
XX PR 30-APR-2002; 2002US-377171P.
XX PA (GETH) GENENTECH INC.
XX PI Dixit V, Grewal I, Ridgway J, Yan M;
XX DR WPI; 2003-248010/25.
XX DR N-PSDB; ABZ68876.
XX PT New nucleic acid encoding a TAC1s or BR3 polypeptide, useful for
PT preparing a composition for treating systemic lupus erythematosus -
XX Disclousure; Fig 9A; 153pp; English.
XX PS The present sequence represents a murine BR3 polypeptide. The
CC specification also describes TAC1 polypeptides. TAC1 and BR3 are
CC receptors. Tumour necrosis factor (TNF) family ligands TALL-1 and
CC April bind to the TAC1 receptor, while TNF family ligands TALL-1 also
CC binds to BR3 receptor. The TAC1 and BR3 receptor nucleic acid is useful
CC for preparing a composition for treating systemic lupus erythematosus.
XX SQ Sequence 175 AA;
Query Match 100.0%; Score 907; DB 24; Length 175;
Best Local Similarity 100.0%; Pred. NO. 5.4e-87;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MGARRLRVRSQRSDSSVPTQCQTECFDPLVNCVSCSELFHTPDGHTSSLEPGTALQP 60
Db 1 MGARRLRVRSQRSDSSVPTQCQTECFDPLVNCVSCSELFHTPDGHTSSLEPGTALQP 60
Qy 61 QEGSALRPDVALLVGAPALLGLILALTIVGLVSLVSWRWQRQLRTASPDTSSEGVQOESLE 120
Db 61 QEGSALRPDVALLVGAPALLGLILALTIVGLVSLVSWRWQRQLRTASPDTSSEGVQOESLE 120
Qy 121 NVFVPSSETPHASAPTWPLKEDADSDALPHRSVVPVDPATELGSTELVTTKTAGEPQ 175
Db 121 NVFVPSSETPHASAPTWPLKEDADSDALPHRSVVPVDPATELGSTELVTTKTAGEPQ 175
Qy 121 NVFVPSSETPHASAPTWPLKEDADSDALPHRSVVPVDPATELGSTELVTTKTAGEPQ 175
Db 121 NVFVPSSETPHASAPTWPLKEDADSDALPHRSVVPVDPATELGSTELVTTKTAGEPQ 175
RESULT 4
ABB78398
ID ABB78398 standard; Protein; 175 AA.
XX AC ABB78398;
XX DT 17-DEC-2002 (first entry)

XX DE Amino acid sequence of murine TRAF3-binding B cell-specific receptor.
XX KW Mouse; TRAF3-binding B cell-specific receptor; TRAF3;
KW signal transduction; TNF ligand; cancer; autoimmune disease; apoplexia;
KW viral infection; AIDS; bone disease; transplantation rejection;
KW Alzheimer's disease; ischaemia; rheumatoid arthritis; cachexia.
XX OS Mus sp.
XX PN WO200272827-A1.
XX PD 19-SEP-2002.
XX PF 28-FEB-2002; 2002WO-JP01849.
XX PR 28-FEB-2001; 2001JP-0055119.
XX PA (RIKE) RIKEN KK.
PA (IRIE/) IRIE S.
PA (SATO/) SATO T.
XX PI Irie S, Sato T;
XX WPI: 2002-713516/77.
XX DR N-PSDB; ABV72373.
XX PT TRAF3-binding B cell-specific receptor and encoded gene, applicable in
PT diagnosis of abnormality due to TRAF3-mediated intracellular signal
PT transduction and in screening drugs for e.g. cancer, autoimmune
PT diseases and AIDS -
XX Claim 1; Page 47-48; 57pp; Japanese.
XX CC The present sequence represents a murine TRAF3-binding B cell-specific
CC receptor. The polynucleotide and polypeptide sequence of this receptor
CC are useful for diagnosis of abnormality due to TRAF3-mediated
CC intracellular signal transduction and in screening drugs for diseases
CC associated with TNF ligand family and TNF receptor-ligand superfamily
CC e.g. cancer, autoimmune diseases, viral infections like AIDS, bone
CC diseases, transplantation rejection, Alzheimer's disease, ischaemia,
CC rheumatoid arthritis, apoplexia and cachexia.
XX SQ Sequence 175 AA;
Query Match 99.4%; Score 902; DB 23; Length 175;
Best Local Similarity 99.4%; Pred. NO. 1.8e-86;
Matches 174; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MGARRLRVRSQRSDSSVPTQCQTECFDPLVNCVSCSELFHTPDGHTSSLEPGTALQP 60
Db 1 MGARRLRVRSQRSDSSVPTQCQTECFDPLVNCVSCSELFHTPDGHTSSLEPGTALQP 60
Qy 61 QEGSALRPDVALLVGAPALLGLILALTIVGLVSLVSWRWQRQLRTASPDTSSEGVQOESLE 120
Db 61 QEGSALRPDVALLVGAPALLGLILALTIVGLVSLVSWRWQRQLRTASPDTSSEGVQOESLE 120
Qy 121 NVFVPSSETPHASAPTWPLKEDADSDALPHRSVVPVDPATELGSTELVTTKTAGEPQ 175
Db 121 NVFVPSSETPHASAPTWPLKEDADSDALPHRSVVPVDPATELGSTELVTTKTAGEPQ 175
RESULT 5
AAE22266
ID AAE22266 standard; Protein; 185 AA.
XX AAE22266;
XX AC AAE22266;
XX DT 25-JUL-2002 (first entry)
XX DE Human BAFF receptor (BAFF-R) mutant, V20N/P21Q/A22T/L27P.
XX KW Human; BAFF receptor; BAFF-R; cytostatic; hypotensive; inflammation; TNF;

XX The invention relates to human BAFF receptor (BAFF-R) nucleic acids and
 CC proteins. BAFF-R is a B-cell activating factor belonging to the Tumour
 CC Necrosis Factor (TNF) family, which is associated with the expression of
 CC B-cells and immunoglobulins. The BAFF-R proteins, DNA and antibodies are
 CC useful for treating, preventing or delaying autoimmune diseases, cancer,
 CC tumorigenic conditions or inherited genetic disorders involving B-cells,
 CC hypertension, cardiovascular disorders, immunosuppressive diseases, renal
 CC disorders, inflammation, organ transplantation and HIV. Autoimmune
 CC diseases, which can be treated or prevented by BAFF-R, include systemic
 CC lupus erythematosus, rheumatoid arthritis, myasthenia gravis, autoimmune
 CC haemolytic anaemia, idiopathic thrombocytopenia purpura, Chagas' disease
 CC Grave's disease, anti-phospholipid syndrome, Wegener's granulomatosis,
 CC poly-arthritis nodosa and rapidly progressive glomerulonephritis. Plasma
 CC cells disorders e.g., multiple myeloma, Waldenström's macroglobulinaemia,
 CC monoclonal gammopathy of undetermined significance. The nucleic acids,
 CC protein, protein homologues, and antibodies may further be used in
 CC screening assays, in detection assays (chromosomal mapping, tissue typing
 CC or forensic biology), predictive medicine (e.g. diagnostic or prognostic
 CC assays, monitoring clinical trials, or pharmacogenomic). The polypeptides
 CC are further useful as immunogens to raise anti-BAFF-R antibodies, or in
 CC screening drugs or compounds that modulate BAFF-R activity or expression.
 CC The present sequence is human BAFF-R protein mutant.
 CC Note: The present sequence is not shown in the specification but is
 CC derived from human BAFF-R referred as SEQ ID NO: 5 (AAE22242) and shown
 CC in fig 2d of the specification.

XX Sequence 185 AA;

Query Match 48.2%; Score 437; DB 23; Length 185;
 Best Local Similarity 58.0%; Pred. No. 1.3e-37;
 Matches 105; Conservative 9; Mismatches 51; Indels 16; Gaps 6;
 QY 9 RSORSDDSVPTCNOTCEFDPLVRNCVSCLEFHP---DTGHTSSLRPGTALQPE--- 62
 DB 6 RSLGRDAPPTPCNTECFDPLVRNCVSCLEFHP---DTGHTSSLRPGTALQPE--- 62
 QY 63 ---GSALRPDVALVGPALLGLILALTIVGLVSLVSWRWQ-QLRTAS----PDTSEGV 114
 DB 66 AGAGEAALPLPGLLFGAPALLGLIALVLAIV-LVGLVSWRRQRRLRGASSAEPDGDKDA 124
 QY 115 QOESLENVFVPSSTPHASAPTPPLKEDADALPHSVFVPATELGSELVTTKTAGE 174
 DB 125 -PEPLDKVILSPGISDATAPAWPPPPGDPGTPPGHSVFPATELGSELVTTKTAGE 183
 QY 175 Q 175
 DB 184 Q 184

RESULT 7
 AAE22269
 ID AAE22269 standard; Protein, 185 AA.

AC AAE22269;

XX 25-JUL-2002 (first entry)

DE Human BAFF receptor (BAFF-R) mutant, V20N/P21Q.

XX Human; BAFF receptor; BAFF-R; cytostatic; hypotensive; inflammatory; TNF;
 KW Tumour Necrosis Factor; autoimmune disease; immunosuppressive; cancer;
 KW myasthenia gravis; hypertension; organ transplantation; drug screening;
 KW HIV; human immunodeficiency virus; genetic disorder; cardiovascular;
 KW renal; rheumatoid arthritis; systemic lupus erythematosus; amyloidosis;
 KW haemolytic anaemia; Chagas' disease; Grave's disease; glomerulonephritis;
 KW multiple myeloma; chromosomal mapping; tissue typing; drug screening;
 KW mutant; mutein.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 20 /note= "Wild type Val substituted with Asn"
 FT FT Misc-difference 21 /note= "Wild type Pro substituted with Gln"
 XX WO2002224909-A2.
 XX 28-MAR-2002.
 XX 06-SEP-2001; 2001WO-US28006.
 XX 18-SEP-2000; 2000US-233152P.
 XX 21-SEP-2000; 2000US-234140P.
 XX 13-FEB-2001; 2001US-268499P.
 XX 14-AUG-2001; 2001US-312185P.
 XX (BIOJ) BIOGEN INC.
 XX Ambrose CM, Thompson JS;
 XX WPI; 2002-362428/39.
 XX New human BAFF receptor proteins and nucleic acids, useful for
 FT treating, preventing or delaying e.g. autoimmune diseases, cancers,
 FT inherited genetic disorders involving B-cells, cardiovascular
 FT disorders, or renal disorders -
 XX Example 17; Page -; 164pp; English.
 XX The invention relates to human BAFF receptor (BAFF-R) nucleic acids and
 CC proteins. BAFF-R is a B-cell activating factor belonging to the Tumour
 CC Necrosis Factor (TNF) family, which is associated with the expression of
 CC B-cells and immunoglobulins. The BAFF-R proteins, DNA and antibodies are
 CC useful for treating, preventing or delaying autoimmune diseases, cancer,
 CC tumorigenic conditions or inherited genetic disorders involving B-cells,
 CC hypertension, cardiovascular disorders, immunosuppressive diseases, renal
 CC disorders, inflammation, organ transplantation and HIV. Autoimmune
 CC diseases, which can be treated or prevented by BAFF-R, include systemic
 CC lupus erythematosus, rheumatoid arthritis, myasthenia gravis, autoimmune
 CC haemolytic anaemia, idiopathic thrombocytopenia purpura, Chagas' disease
 CC Grave's disease, anti-phospholipid syndrome, Wegener's granulomatosis,
 CC poly-arthritis nodosa and rapidly progressive glomerulonephritis. Plasma
 CC cells disorders e.g., multiple myeloma, Waldenström's macroglobulinaemia,
 CC heavy-chain disease, primary or immunocyte-associated amyloidosis, and
 CC monoclonal gammopathy of undetermined significance. The nucleic acids,
 CC protein, protein homologues, and antibodies may further be used in
 CC screening assays, in detection assays (chromosomal mapping, tissue typing
 CC or forensic biology), predictive medicine (e.g. diagnostic or prognostic
 CC assays, monitoring clinical trials, or pharmacogenomic). The polypeptides
 CC are further useful as immunogens to raise anti-BAFF-R antibodies, or in
 CC screening drugs or compounds that modulate BAFF-R activity or expression.
 CC The present sequence is human BAFF-R protein mutant.
 CC Note: The present sequence is not shown in the specification but is
 CC derived from human BAFF-R referred as SEQ ID NO: 5 (AAE22242) and shown
 CC in fig 2d of the specification.

XX Sequence 185 AA;

Query Match 47.6%; Score 432; DB 23; Length 185;
 Best Local Similarity 57.5%; Pred. No. 4.4e-37;
 Matches 104; Conservative 9; Mismatches 52; Indels 16; Gaps 6;
 QY 9 RSORSDDSVPTCNOTCEFDPLVRNCVSCLEFHP---DTGHTSSLRPGTALQPE--- 62
 DB 6 RSLGRDAPPTPCNTECFDPLVRNCVSCLEFHP---DTGHTSSLRPGTALQPE--- 62
 QY 63 ---GSALRPDVALVGPALLGLILALTIVGLVSLVSWRWQ-QLRTAS----PDTSEGV 114
 DB 66 AGAGEAALPLPGLLFGAPALLGLIALVLAIV-LVGLVSWRRQRRLRGASSAEPDGDKDA 124
 QY 115 QOESLENVFVPSSTPHASAPTPPLKEDADALPHSVFVPATELGSELVTTKTAGE 174
 DB 125 -PEPLDKVILSPGISDATAPAWPPPPGDPGTPPGHSVFPATELGSELVTTKTAGE 183

QY 175 Q 175
Db 184 Q 184

RESULT 8
AAE22268
ID AAE22268 standard; Protein; 185 AA.
XX
XX AAE22268;
XX
XX 25-JUL-2002 (first entry)
XX
XX Human BAFF receptor (BAFF-R) mutant, V20N/A22T.
XX
XX Human; BAFF receptor; BAFF-R; cytostatic; hypotensive; inflammation; TNF;
KW Tumour Necrosis Factor; autoimmune disease; immunosuppressive; cancer;
KW myasthenia gravis; hypertension; organ transplantation; drug screening;
KW HIV; human immunodeficiency virus; genetic disorder; cardiovascular;
KW renal; rheumatoid arthritis; systemic lupus erythematosus; amyloidosis;
KW haemolytic anaemia; Chagas' disease; Grave's disease; glomerulonephritis;
KW multiple myeloma; chromosomal mapping; tissue typing; drug screening;
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Misc-difference 20
FT Misc-difference 22 /note= "Wild type Val substituted with Asn"
FT Misc-difference 22 /note= "Wild type Ala substituted with Thr"
FT
FT
XX WO200224909-A2.
XX
XX 28-MAR-2002.
XX
XX 06-SEP-2001; 2001WO-US28006.
XX
XX 18-SEP-2000; 2000US-233152P.
XX 21-SEP-2000; 2000US-234140P.
XX 13-FEB-2001; 2001US-268499P.
XX 14-AUG-2001; 2001US-312185P.
XX
XX (BIOJ) BIOGEN INC.
XX
XX Ambrose CM, Thompson JS;
XX
XX WPI; 2002-362428/39.
XX
XX New human BAFF receptor proteins and nucleic acids, useful for
PT treating, preventing or delaying e.g. autoimmune diseases, cancers,
PT inherited genetic disorders involving B-cells, cardiovascular
PT disorders, or renal disorders -
XX
XX Example 17; Page -; 164pp; English.
XX
XX The invention relates to human BAFF receptor (BAFF-R) nucleic acids and
XX proteins. BAFF-R is a B-cell activating factor belonging to the Tumour
XX Necrosis Factor (TNF) family, which is associated with the expression of
XX B-cells and immunoglobulins. The BAFF-R proteins, DNA and antibodies are
XX useful for treating, preventing or delaying autoimmune diseases, cancer,
XX tumorigenic conditions or inherited genetic disorders involving B-cells,
XX hyperension, cardiovascular disorders, immunosuppressive diseases, renal
XX disorders, inflammation, organ transplantation and HIV. Autoimmune
XX diseases, which can be treated or prevented by BAFF-R, include systemic
XX lupus erythematosus, rheumatoid arthritis, myasthenia gravis, autoimmune
XX haemolytic anaemia, idiopathic thrombocytopenia purpura, Chagas' disease
XX Grave's disease, anti-phospholipid syndrome, Wegener's granulomatosis,
XX poly-arthritis nodosa and rapidly progressive glomerulonephritis. Plasma
XX cells disorders e.g., multiple myeloma, Waldenström's macroglobulinaemia,
XX heavy-chain disease, primary or immunocyte-associated amyloidosis, and
XX monoclonal gammopathy of undetermined significance. The nucleic acids,

CC protein, protein homologues, and antibodies may further be used in
CC screening assays, in detection assays (chromosomal mapping, tissue typing
CC or forensic biology), predictive medicine (e.g. diagnostic or prognostic
CC assays, monitoring clinical trials, or pharmacogenomic). The polypeptides
CC are further useful as immunogens to raise anti-BFFR antibodies, or in
CC screening drugs or compounds that modulate BAFF-R activity or expression.
CC The present sequence is human BAFF-R protein mutant.
CC Note: The present sequence is not shown in the specification but is
CC derived from human BAFF-R referred as SEQ ID NO: 5 (AAE22242) and shown
CC in fig 2d of the specification.
XX
XX Sequence 185 AA;
SQ

Query Match 47.5%; Score 431; DB 23; Length 185;
Best Local Similarity 57.5%; Pred. No. 5.5e-37;
Matches 104; Conservative 9; Mismatches 52; Indels 16; Gaps 6;
QY 9 RSQRSDSVFTQCNOTCFDPLVNCVSCLEFHTP---DTGHTSLBFGTALQPOE--- 62
Db 6 RSLRGDAPAPTCTNTECFDPLVNCVSCLEFHTP---DTGHTSLBFGTALQPOE--- 65
QY 63 ---GSLRPDVALVCAPALLGLILALTAVGLVSLVSWRWQ-QLRTAS---PDTSEGV 114
Db 66 AGAGEAALPLGLFAPALLGLALVLAIV-LVGLVSWRRRRRLRGASSAEPDGDKA 124
QY 115 QBSLENVFPVSSETPHASPTWPKEDADSALPRHSVPVPATLSTELVTTKTAGE 174
Db 125 -PEPLDKVILSPGISDATAPAWPPPGEDPTTPPGHSPVPATLSTELVTTKTAGE 183
QY 175 Q 175
Db 184 Q 184

RESULT 9
AAE22270
ID AAE22270 standard; Protein; 185 AA.
XX
XX AC AAE22270;
XX
XX 25-JUL-2002 (first entry)
XX
XX Human BAFF receptor (BAFF-R) mutant, V20N.
XX
XX Human; BAFF receptor; BAFF-R; cytostatic; hypotensive; inflammation; TNF;
KW Tumour Necrosis Factor; autoimmune disease; immunosuppressive; cancer;
KW myasthenia gravis; hypertension; organ transplantation; drug screening;
KW HIV; human immunodeficiency virus; genetic disorder; cardiovascular;
KW renal; rheumatoid arthritis; systemic lupus erythematosus; amyloidosis;
KW haemolytic anaemia; Chagas' disease; Grave's disease; glomerulonephritis;
KW multiple myeloma; chromosomal mapping; tissue typing; drug screening;
KW mutant; mutein.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Misc-difference 20 /note= "Wild type Val substituted with Asn"
FT
XX WO200224909-A2.
XX 28-MAR-2002.
XX 06-SEP-2001; 2001WO-US28006.
XX 18-SEP-2000; 2000US-233152P.
XX 21-SEP-2000; 2000US-234140P.
XX 13-FEB-2001; 2001US-268499P.
XX 14-AUG-2001; 2001US-312185P.
XX
XX (BIOJ) BIOGEN INC.
XX
XX Ambrose CM, Thompson JS;
XX
XX WPI; 2002-362428/39.
XX
XX New human BAFF receptor proteins and nucleic acids, useful for
PT treating, preventing or delaying e.g. autoimmune diseases, cancers,
PT inherited genetic disorders involving B-cells, cardiovascular
PT disorders, or renal disorders -
XX
XX Example 17; Page -; 164pp; English.
XX
XX The invention relates to human BAFF receptor (BAFF-R) nucleic acids and
XX proteins. BAFF-R is a B-cell activating factor belonging to the Tumour
XX Necrosis Factor (TNF) family, which is associated with the expression of
XX B-cells and immunoglobulins. The BAFF-R proteins, DNA and antibodies are
XX useful for treating, preventing or delaying autoimmune diseases, cancer,
XX tumorigenic conditions or inherited genetic disorders involving B-cells,
XX hyperension, cardiovascular disorders, immunosuppressive diseases, renal
XX disorders, inflammation, organ transplantation and HIV. Autoimmune
XX diseases, which can be treated or prevented by BAFF-R, include systemic
XX lupus erythematosus, rheumatoid arthritis, myasthenia gravis, autoimmune
XX haemolytic anaemia, idiopathic thrombocytopenia purpura, Chagas' disease
XX Grave's disease, anti-phospholipid syndrome, Wegener's granulomatosis,
XX poly-arthritis nodosa and rapidly progressive glomerulonephritis. Plasma
XX cells disorders e.g., multiple myeloma, Waldenström's macroglobulinaemia,
XX heavy-chain disease, primary or immunocyte-associated amyloidosis, and
XX monoclonal gammopathy of undetermined significance. The nucleic acids,

XX WPI; 2002-362428/39.
XX
XX New human BAFF receptor proteins and nucleic acids, useful for
PT treating, preventing or delaying e.g. autoimmune diseases, cancers,
PT inherited genetic disorders involving B-cells, cardiovascular
PT disorders, or renal disorders -
XX
XX Example 17; Page -: 164pp; English.
XX
XX The invention relates to human BAFF receptor (BAFF-R) nucleic acids and
CC proteins. BAFF-R is a B-cell activating factor belonging to the Tumour
CC Necrosis Factor (TNF) family, which is associated with the expression of
CC B-cells and immunoglobulins. The BAFF-R proteins, DNA and antibodies are
CC useful for treating, preventing or delaying autoimmune diseases, cancer,
CC tumorigenic conditions or inherited genetic disorders involving B-cells,
CC hyperinflammation, cardiovascular disorders, immunosuppressive diseases, renal
CC disorders, inflammation, organ transplantation and HIV. Autoimmune
CC diseases, which can be treated or prevented by BAFF-R, include systemic
CC lupus erythematosus, rheumatoid arthritis, myasthenia gravis, autoimmune
CC haemolytic anaemia, idiopathic thrombocytopenia purpura, Chagas' disease
CC Grave's disease, anti-phospholipid syndrome, Wegener's granulomatosis,
CC poly-arthritis nodosa and rapidly progressive glomerulonephritis. Plasma
CC cells disorders e.g., multiple myeloma, Waldenström's macroglobulinaemia,
CC heavy-chain gammopathy of undetermined significance. The nucleic acids,
CC protein, protein homologues, and antibodies may further be used in
CC screening assays, in detection assays (chromosomal mapping, tissue typing
CC or forensic biology), predictive medicine (e.g. diagnostic or prognostic
CC assays, monitoring clinical trials, or pharmacogenomic). The polypeptides
CC are further useful as immunogens to raise anti-BAFF-R antibodies, or in
CC screening drugs or compounds that modulate BAFF-R activity or expression.
CC The present sequence is human BAFF-R protein mutant.
CC Note: The present sequence is not shown in the specification but is
CC derived from human BAFF-R referred as SEQ ID NO: 5 (AAE22242) and shown
CC in fig 2d of the specification.
XX
XX Sequence 185 AA;
XX
XX Query Match 47.0%; Score 426; DB 23; Length 185;
XX Best Local Similarity 56.9%; Pred. No. 1.9e-36;
XX Matches 103; Conservative 9; Mismatches 53; Indels 16; Gaps 6;
XX
QY 9 RSQRSDSVPTQCNQTECFDPLVNCVSCELFHTP---DTGHTSSLEPPTALQPE--- 62
DB 6 RSLRGDAPAPTEPCVQACFCDDLVRHCVACGLLRTPPKPAGAASSPAPRTALQPESVG 65
QY 63 ---GSALRPDVALVGPAPALLGLILALTILVGLVLSVSWRWQ-QLRTAS---PDTSEGV 114
DB 66 AGAGEAALPLPGLLFGAPALLGLALVLAIV-LVGLVSWRRQRRLRGSSAEPDGDKA 124
QY 115 QQESLENVFPSSETHASAPTPWPLKEDASALPRHSVPVPATELGSTELVTTKTAGE 174
DB 125 -PEPLDKVILSPGISDATAPAWPPFGEDPGTTPPGHVSFVZPATELGSTELVTTKTAGE 183
QY 175 Q 175
DB 184 Q 184
RESULT 10
ID AAE22271 standard; Protein; 185 AA.
XX
XX AAE22271;
XX
XX 25-JUL-2002 (first entry)
XX
XX Human BAFF receptor (BAFF-R) mutant, P21Q.
XX
XX Human; BAFF receptor; BAFF-R; cytototoxic; hypotensive; inflammation; TNF;
KW Tumour Necrosis Factor; autoimmune disease; immunosuppressive; cancer;
KW myasthenia gravis; hypertension; organ transplantation; drug screening;

KW HIV; human immunodeficiency virus; genetic disorder; cardiovascular;
KW renal; rheumatoid arthritis; systemic lupus erythematosus; amyloidosis;
KW haemolytic anaemia; Chagas' disease; Grave's disease; glomerulonephritis;
KW multiple myeloma; chromosomal mapping; tissue typing; drug screening;
XX mutant; mutein.
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FT Misc-difference 21 /note= "Wild type Pro substituted with Gln"
XX
XX WO200224909-A2.
XX
XX 28-MAR-2002.
XX
XX 06-SEP-2001; 2001WO-US28006.
XX
XX 18-SEP-2000; 2000US-233152P.
XX 21-SEP-2000; 2000US-234140P.
XX 13-FEB-2001; 2001US-268499P.
XX 14-AUG-2001; 2001US-312185P.
XX
XX (BIOJ) BIOGEN INC.
XX
XX Ambrose CM, Thompson JS;
XX
XX WPI; 2002-362428/39.
XX
XX New human BAFF receptor proteins and nucleic acids, useful for
PT treating, preventing or delaying e.g. autoimmune diseases, cancers,
PT inherited genetic disorders involving B-cells, cardiovascular
PT disorders, or renal disorders -
XX
XX Example 17; Page -: 164pp; English.
XX
XX The invention relates to human BAFF receptor (BAFF-R) nucleic acids and
CC proteins. BAFF-R is a B-cell activating factor belonging to the Tumour
CC Necrosis Factor (TNF) family, which is associated with the expression of
CC B-cells and immunoglobulins. The BAFF-R proteins, DNA and antibodies are
CC useful for treating, preventing or delaying autoimmune diseases, cancer,
CC tumorigenic conditions or inherited genetic disorders involving B-cells,
CC hypertension, cardiovascular disorders, immunosuppressive diseases, renal
CC disorders, inflammation, organ transplantation and HIV. Autoimmune
CC diseases, which can be treated or prevented by BAFF-R, include systemic
CC lupus erythematosus, rheumatoid arthritis, myasthenia gravis, autoimmune
CC haemolytic anaemia, idiopathic thrombocytopenia purpura, Chagas' disease
CC Grave's disease, anti-phospholipid syndrome, Wegener's granulomatosis,
CC poly-arthritis nodosa and rapidly progressive glomerulonephritis. Plasma
CC cells disorders e.g., multiple myeloma, Waldenström's macroglobulinaemia,
CC heavy-chain gammopathy of undetermined significance. The nucleic acids,
CC protein, protein homologues, and antibodies may further be used in
CC screening assays, in detection assays (chromosomal mapping, tissue typing
CC or forensic biology), predictive medicine (e.g. diagnostic or prognostic
CC assays, monitoring clinical trials, or pharmacogenomic). The polypeptides
CC are further useful as immunogens to raise anti-BAFF-R antibodies, or in
CC screening drugs or compounds that modulate BAFF-R activity or expression.
CC The present sequence is human BAFF-R protein mutant.
CC Note: The present sequence is not shown in the specification but is
CC derived from human BAFF-R referred as SEQ ID NO: 5 (AAE22242) and shown
CC in fig 2d of the specification.
XX
XX Sequence 185 AA;
XX
XX Query Match 46.6%; Score 423; DB 23; Length 185;
XX Best Local Similarity 56.9%; Pred. No. 3.8e-36;
XX Matches 103; Conservative 9; Mismatches 53; Indels 16; Gaps 6;
XX
QY 9 RSQRSDSVPTQCNQTECFDPLVNCVSCELFHTP---DTGHTSSLEPPTALQPE--- 62
DB 6 RSLRGDAPAPTEPCVQACFCDDLVRHCVACGLLRTPPKPAGAASSPAPRTALQPESVG 65

QY 63 ---GSALRPDVALVGPALLGLILALTLVGLVSLVSWRWQ-QLETS-PTSEGV 114
 Db 66 AGAGEAALPLPLGLFGAPALLGLALVLAIV-LVGLVSWRRQRRLRGASSAEPDGDKA 124
 QY 115 QOESLENVFPSSSTPHASAPTWPLKEDADSDALPRHSVVPVPA TELGSGTELVTTKTAGE 174
 Db 125 -PEFLDKVIIISPGISDATAPAMPWPPGDEGTPPGHSVVPVPA TELGSGTELVTTKTAGE 183
 QY 175 Q 175
 Db 184 Q 184

RESULT 11
 AAE22242
 ID AAE22242 standard; Protein; 185 AA.
 AC AAE22242;
 DT 25-JUL-2002 (first entry)
 XX Human mature JST576 (BAFF-R) protein.
 KW Human; BAFF receptor; BAFF-R; cytostatic; hypotensive; inflammation; TNF;
 KW Tumour Necrosis Factor; autoimmune disease; immunosuppressive; cancer;
 KW myasthenia gravis; hypertension; organ transplantation; drug screening;
 KW HIV; human immunodeficiency virus; genetic disorder; cardiovascular;
 KW renal; rheumatoid arthritis; systemic lupus erythematosus; amyloidosis;
 KW haemolytic anaemia; Chagas' disease; Grave's disease; glomerulonephritis;
 KW multiple myeloma; chromosomal mapping; tissue typing; drug screening;
 JST576.
 XX Homo sapiens.
 FH Key
 FT Domain
 FT Location/Qualifiers
 FT 19..35
 FT /note= "Four cysteine motif"
 FT Misc-difference 49
 FT /note= "Alternative splice acceptor site"
 FT Region 72..100
 FT /note= "Hydrophobic region"
 FT Domain 73..100
 FT /label= Transmembrane_domain
 FT Region 105..108
 FT /note= "Stop transfer signal"
 FT FT
 XX WO200224909-A2.
 XX PD 28-MAR-2002.
 XX PF 06-SEP-2001; 2001WO-US28006.
 XX PR 18-SEP-2000; 2000US-233152P.
 XX PR 21-SEP-2000; 2000US-234140P.
 XX PR 13-FEB-2001; 2001US-268499P.
 XX PR 14-AUG-2001; 2001US-312185P.
 XX (BIOJ) BIOGEN INC.
 XX Ambrose CM, Thompson JS;
 XX WPI; 2002-362428/39.
 XX N-PSDB; AAD35409.
 XX New human BAFF receptor proteins and nucleic acids, useful for
 FT treating, preventing or delaying e.g. autoimmune diseases, cancers,
 FT inherited genetic disorders involving B-cells, cardiovascular
 FT disorders, or renal disorders
 XX Claim 1; Fig 2d; 164pp; English.
 XX The invention relates to human BAFF receptor (BAFF-R) nucleic acids and
 CC proteins. BAFF-R is a B-cell activating factor belonging to the tumour

CC Necrosis Factor (TNF) family, which is associated with the expression of
 CC B-cells and immunoglobulins. The BAFF-R proteins, DNA and antibodies are
 CC useful for treating, preventing or delaying autoimmune diseases, cancer,
 CC tumorigenic conditions or inherited genetic disorders involving B-cells,
 CC hypertension, cardiovascular disorders, immunosuppressive diseases, renal
 CC disorders, inflammation, organ transplantation and HIV. Autoimmune
 CC diseases, which can be treated or prevented by BAFF-R, include systemic
 CC lupus erythematosus, rheumatoid arthritis, myasthenia gravis, autoimmune
 CC haemolytic anaemia, idiopathic thrombocytopenic purpura, Chagas' disease
 CC Grave's disease, anti-phospholipid syndrome, Wegener's granulomatosis,
 CC poly-arthritis nodosa and rapidly progressive glomerulonephritis. Plasma
 CC cells disorders e.g., multiple myeloma, Waldenstrom's macroglobulinaemia,
 CC heavy-chain disease, primary or immunocyte-associated amyloidosis, and
 CC monoclonal gammopathy of undetermined significance. The nucleic acids,
 CC protein, protein homologues, and antibodies may further be used in
 CC screening assays, in detection assays (chromosomal mapping, tissue typing
 CC or forensic biology), predictive medicine (e.g. diagnostic or prognostic
 CC assays, monitoring clinical trials, or pharmacogenomic). The polypeptides
 CC are further useful as immunogens to raise anti-BPFR antibodies, or in
 CC screening drugs or compounds that modulate BAFF-R activity or expression.
 CC The present sequence is human mature JST576 (BAFF-R) protein.
 XX

Sequence 185 AA;

Query Match 46.0%; Score 417; DB 23; Length 185;
 Best Local Similarity 56.4%; Pred. No. 1.6e-35;
 Matches 102; Conservative 9; Mismatches 54; Indels 16; Gaps 6;

QY 9 RSQRSDSVPTCQNTCEFDPLVRNCVSCLEFHP- ---DGTGTSLEPGTALQPE- - 62

Db 6 RSRGRDAPPTPCVPAECFDLLVRHVACGLRTPRPKAPGAGASSPAPRTALQQESVG 65

QY 63 ---GSALRPDVALVGPALLGLILALTLVGLVSLVSWRWQ-QLETS-PTSEGV 114

Db 66 AGAGEAALPLPLGLFGAPALLGLALVLAIV-LVGLVSWRRQRRLRGASSAEPDGDKA 124

QY 115 QOESLENVFPSSSTPHASAPTWPLKEDADSDALPRHSVVPVPA TELGSGTELVTTKTAGE 174

Db 125 -PEFLDKVIIISPGISDATAPAMPWPPGDEGTPPGHSVVPVPA TELGSGTELVTTKTAGE 183

QY 175 Q 175

Db 184 Q 184

RESULT 12

AAE22243

ID AAE22243 standard; Protein; 266 AA.

AC AAE22243;

DT 25-JUL-2002 (first entry)

Human JST576 (BAFF-R) cDNA spliced version encoded protein.

Human; BAFF receptor; BAFF-R; cytostatic; hypotensive; inflammation; TNF;
 KW Tumour Necrosis Factor; autoimmune disease; immunosuppressive; cancer;
 KW myasthenia gravis; hypertension; organ transplantation; drug screening;
 KW HIV; human immunodeficiency virus; genetic disorder; cardiovascular;
 KW renal; rheumatoid arthritis; systemic lupus erythematosus; amyloidosis;
 KW haemolytic anaemia; Chagas' disease; Grave's disease; glomerulonephritis;
 KW multiple myeloma; chromosomal mapping; tissue typing; drug screening;
 JST576.
 XX Homo sapiens.
 XX WO200224909-A2.
 XX PD 28-MAR-2002.
 XX 06-SEP-2001; 2001WO-US28006.
 XX 18-SEP-2000; 2000US-233152P.

PR 21-SEP-2000; 2000US-234140P.
PR 13-FEB-2001; 2001US-268499P.
PR 14-AUG-2001; 2001US-312185P.

PA (BIOJ) BIOGEN INC.

PI Ambrose CW, Thompson JS;

XX WPI; 2002-362428/39.

DR N-PSDB; AAD35410.

XX New human BAF-R receptor proteins and nucleic acids, useful for
PT treating, preventing or delaying e.g. autoimmune diseases, cancers,
PT inherited genetic disorders involving B-cells, cardiovascular
PT disorders, or renal disorders -

XX Example 3; Fig 3; 164pp; English.

XX The invention relates to human BAF-R receptor (BAF-R) nucleic acids and
CC proteins. BAF-R is a B-cell activating factor belonging to the Tumour
CC Necrosis Factor (TNF) family, which is associated with the expression of
CC B-cells and immunoglobulins. The BAF-R proteins, DNA and antibodies are
CC useful for treating, preventing or delaying autoimmune diseases, cancer,
CC tumorigenic conditions or inherited genetic disorders involving B-cells,
CC hypertension, cardiovascular disorders, immunosuppressive diseases, renal
CC disorders, inflammation, organ transplantation and HIV. Autoimmune
CC diseases, which can be treated or prevented by BAF-R, include systemic
CC lupus erythematosus, rheumatoid arthritis, myasthenia gravis, autoimmune
CC haemolytic anaemia, idiopathic thrombocytopenia purpura, Chagas' disease
CC Grave's disease, anti-phospholipid syndrome, Wegener's granulomatosis,
CC poly-arthritis nodosa and rapidly progressive glomerulonephritis. Plasma
CC cells disorders e.g., multiple myeloma, Waldenström's macroglobulinaemia,
CC heavy-chain disease, primary or immunocyte-associated amyloidosis, and
CC monoclonal gammopathy of undetermined significance. The nucleic acids,
CC protein, protein homologues, and antibodies may further be used in
CC screening assays, in detection assays (chromosomal mapping, tissue typing
CC or forensic biology), predictive medicine (e.g. diagnostic or prognostic
CC assays, monitoring clinical trials, or pharmacogenomic). The polypeptides
CC are further useful as immunogens to raise anti-BAF-R antibodies, or in
CC screening drugs or compounds that modulate BAF-R activity or expression.
CC The present sequence is human mature JST576. (BAF-R) cDNA spliced version
CC containing 5' UTR encoded protein.

XX Sequence 266 AA;

Query Match 45.8%; Score 415.5; DB 23; Length 266;
Best Local Similarity 54.8%; Pred. No. 3.9e-35;
Matches 103; Conservative 10; Mismatches 60; Indels 15; Gaps 6;

QY 1 MGARELRVRSQRSDSSVPTQCNQTECFDPLVRNCVSCLEFHT--PDTGHTSSLEPGTAL 58

DB 80 VGTMRGPRSLRGDRDAPPTCPVAECFDLLVRHCVACGLLRTPRPKAGASSPAPRTAL 139

QY 59 QPQE-----GSALEPDVALLVGAPALIGLTLALTLYGLVLSVWRQ-QLRTAS---- 107

DB 140 QPQESVGAGAGEAALPLGGLFGAPALIGLALVALV-LVGLVSWRRQRRLGASASA 198

QY 108 PPTSSEGVQSELENVFPSSSTPHASAPTWPPLKEDASALPRHSVPVPATLGSTELVT 167

DB 199 PDGKDA-PEPLDKVIIISPGISDAPAWPPPGEDGTTTGGHVSVPVATLGSTELVT 257

QY 168 TKTAGPEQ 175

DB 258 TKTAGPEQ 265

RESULT 13

AB381483

ID ABB81483 standard; Protein; 184 AA.

XX ABB81483;

XX 02-SEP-2002 (first entry)

DT

XX

DB

XX

KW

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KW

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PN

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PD

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PF

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Human Ztnfr12 protein SEQ ID NO:2.

Human; Ztnfr12; tumour necrosis factor receptor; cytotostatic;
immunosuppressive; dermatological; antiinflammatory; antidiabetic;
neuroprotective; antirheumatic; antiarthritic; antiasthmatic;
nephrotropic; hypotensive; gene therapy; B lymphocyte; tumour;
autoimmune disorder; systemic lupus erythematosus; myasthenia gravis;
multiple sclerosis; insulin dependent diabetes mellitus; asthma;
rheumatoid arthritis; bronchitis; emphysema; renal disease; lymphoma;
glomerulonephritis; vasculitis; chronic lymphoid leukaemia; nephritis;
pyelonephritis; renal neoplasm; multiple myeloma; amyloidosis;
light chain neuropathy; hypertension; large vessel disease;
graft-versus host disease; graft rejection; Crohn's disease;
chromosome 22q13.2.

Homo sapiens.

WO200238766-A2.

16-MAY-2002.

05-NOV-2001; 2001WO-US47018.

07-NOV-2000; 2000US-246449P.

20-DEC-2000; 2000US-257131P.

28-JUN-2001; 2001US-301715P.

29-AUG-2001; 2001US-315565P.

(ZYMO) ZYMOGENETICS INC.

Gross JA, Xu W, Henne RM, Grant FJ;

WPI; 2002-508212/54.

N-PSDB; AEN99426.

Novel isolated human tumor necrosis factor receptor polypeptide, termed
Ztnfr 12, useful for treating autoimmune disorders, emphysema, end
stage renal failure or renal disease and lymphoma -

Claim 3; Page 133; 154pp; English.

The present sequence represents a human tumour necrosis factor receptor
designated ztnfr12 (I). (I) has cytostatic, immunosuppressive,
dermatological, antiinflammatory, neuroprotective, antidiabetic,
antirheumatic, antiarthritic, antiasthmatic, nephrotropic and hypotensive
activities, and can be used in gene therapy. (I) can be used for
inhibiting, in a mammal, the activity of a ligand that binds Ztnfr12
(e.g. Ztnfr4), for treating disorders and diseases associated with B
lymphocytes, activated B lymphocytes or resting B lymphocytes, and for
inhibiting the proliferation of tumour cells. (I) is useful for treating
autoimmune disorders such as systemic lupus erythematosus, myasthenia
gravis, multiple sclerosis, insulin dependent diabetes mellitus, asthma,
rheumatoid arthritis, bronchitis, emphysema and end stage renal failure
or renal disease such as glomerulonephritis, vasculitis, chronic lymphoid
leukaemia, nephritis, and pyelonephritis, and for treating renal
neoplasms, multiple myelomas, lymphomas, light chain neuropathy, or
amyloidosis, hypertension, large vessel diseases, graft-versus host
disease, graft rejection and Crohn's disease. (I) is useful for
modulating the immune system, for regulating B cell responses and
development, for modulating development of other cells, antibody
production and cytokine production, and for modulating T and B cell
communication. Human Ztnfr12 is located to chromosome 22q13.2.

Sequence 184 AA;

Query Match 45.3%; Score 410.5; DB 23; Length 184;

Best Local Similarity 56.1%; Pred. No. 7.8e-35;

Matches 101; Conservative 9; Mismatches 55; Indels 15; Gaps 6;

QY 9 RSQRSRDSSVPTQCNQTECFDPLVRNCVSCLEFHT--PDTGHTSSLEPGTALQPQE---- 62

DB 6 RSLRGDRAPPTCPVAECFDLLVRHCVACGLLRTPRPKAGASSPAPRTALQPQESVGA 65

QY 63 --GSALRPDVALVGPALLGLILALTLVGLVSLVSWRWQ-QLRTAS----PDTSEGVQ 115
 Db 66 GAGEAALPLPGLLFGAPALLGLALVLAIV-LVGLVSWRWQRRLRGASSAEPDGDKDA- 123
 QY 116 QESLENVFPVSSETPHASAPTWPKEDADSALPRHSVPVPATELGSTELVTTKTAGEPQ 175
 Db 124 PEPLDKVILLSPG:SDATAPAWPPGPDGPTTPPGHSVPVPATELGSTELVTTKTAGEPQ 183

RESULT 14
 AAE35227
 ID AAE35227 standard; Protein; 184 AA.
 XX AAE35227;
 AC AAE35227;
 DT 28-MAY-2003 (first entry)
 XX Human Ztnfr12 receptor protein.
 DE
 XX Transmembrane activator; calcium modulator; nephrotropic; antibacterial;
 KW TAC1; tumour necrosis factor-like protein; ZTNF2; ZTNF4; immunoglobulin;
 KW anaemia; gene therapy; cytostatic; antiinflammatory; immunosuppressive;
 KW glomerulonephritis; asthma; bronchitis; graft rejection; septic shock;
 KW dermatological; neuroprotective; cyclophilin ligand-interactor; human;
 KW autoimmune disease; systemic lupus erythematosus; multiple sclerosis;
 KW diabetes mellitus; rheumatoid arthritis; renal disease; inflammation;
 KW Ztnfr12; receptor.
 XX
 OS Homo sapiens.
 XX WO200294852-A2.
 PN 28-NOV-2002.
 XX
 PD 20-MAY-2002; 2002WO-US15910.
 PF 20-MAY-2001; 2001US-293343P.
 PR 24-MAY-2001; 2001US-293343P.
 XX (ZYMO) ZYMOGENETICS INC.
 PA Rixon MW, Gross JA;
 PI WPI; 2003-148455/14.
 XX N-PSDB; AAD53776.
 DR Transmembrane activator and calcium modulator and cyclophilin
 PT ligand-interactor (TAC1)-immunoglobulin fusion protein, for treating
 PT cancer or diabetes, comprises a TAC1 receptor group and an
 PT immunoglobulin group -
 XX Disclosure; Column 136-137; 71pp; English.
 PS The invention relates to fusion proteins comprising transmembrane
 XX activator and calcium modulator and cyclophilin ligand-interactor (TAC1)
 CC receptor group that binds tumour necrosis factor-like protein (ZTNF)2 or
 CC ZTNF4; and an immunoglobulin group comprising a constant region of an
 CC immunoglobulin. The invention is used to manufacture a medicament for
 CC inhibiting the proliferation of tumour cells in a mammalian subject.
 CC The composition comprising the fusion protein may also be used in
 CC treating autoimmune diseases (e.g. systemic lupus erythematosus,
 CC multiple sclerosis, diabetes mellitus, rheumatoid arthritis and asthma),
 CC renal diseases (e.g. glomerulonephritis), bronchitis, inflammation,
 CC graft rejection, anaemia and septic shock. The fusion proteins are
 CC also used in gene therapy. The present sequence is human Ztnfr12
 CC receptor protein.
 XX
 XX Sequence 184 AA;
 Query Match 45.3%; Score 410.5; DB 24; Length 184;
 Best Local Similarity 56.1%; Pred. No. 7.8e-35;
 Matches 101; Conservative 9; Mismatches 55; Indels 15; Gaps 6;

QY 9 RSORSRDSVPTQCNTQCEFDPLVRNCVSCELFHT--PDTGHTSSLBPGTALQPOE---- 62
 Db 6 RSLRGRDAPAPTCPVAECFDLLVRHCVACGLLRTPRPKPAGASSPAPRTALQPOESVGA 65
 QY 63 --GSALRPDVALVGPALLGLILALTLVGLVSLVSWRWQ-QLRTAS----PDTSEGVQ 115
 Db 66 GAGEAALPLPGLLFGAPALLGLALVLAIV-LVGLVSWRWQRRLRGASSAEPDGDKDA- 123
 QY 116 QESLENVFPVSSETPHASAPTWPKEDADSALPRHSVPVPATELGSTELVTTKTAGEPQ 175
 Db 124 PEPLDKVILLSPG:SDATAPAWPPGPDGPTTPPGHSVPVPATELGSTELVTTKTAGEPQ 183

RESULT 15
 ABP97721
 ID ABP97721 standard; Protein; 184 AA.
 XX ABP97721;
 AC ABP97721;
 DT 28-MAY-2003 (first entry)
 XX Amino acid sequence of human BR3 receptor.
 DE Human; TAC1; BR3; receptor; tumour necrosis factor ligand; TNF ligand;
 KW TALL-1; April; systemic lupus erythematosus.
 XX Homo sapiens.
 OS WO2003014294-A2.
 PN 20-FEB-2003.
 XX
 PD 24-JUL-2002; 2002WO-US23487.
 PF 03-AUG-2001; 2001US-310114P.
 PR 30-APR-2002; 2002US-37717P.
 XX (GETH) GENENTECH INC.
 PA Dixit V, Grewal I, Ridgway J, Yan M;
 PI WPI; 2003-248010/25.
 XX New nucleic acid encoding a TAC1s or BR3 polypeptide, useful for
 PT preparing a composition for treating systemic lupus erythematosus -
 XX Claim 35; Fig 6B; 153pp; English.
 PS The present sequence represents a human BR3 polypeptide. The
 CC specification also describes TAC1 polypeptides. TAC1 and BR3 are
 CC receptors. Tumour necrosis factor (TNF) family ligands TALL-1 and
 CC April bind to the TAC1 receptor, while TNF family ligands TALL-1 also
 CC binds to BR3 receptor. The TAC1 and BR3 receptor nucleic acid is useful
 CC for preparing a composition for treating systemic lupus erythematosus.
 XX Sequence 184 AA;
 Query Match 45.3%; Score 410.5; DB 24; Length 184;
 Best Local Similarity 56.1%; Pred. No. 7.8e-35;
 Matches 101; Conservative 9; Mismatches 55; Indels 15; Gaps 6;

QY 9 RSORSRDSVPTQCNTQCEFDPLVRNCVSCELFHT--PDTGHTSSLBPGTALQPOE---- 62
 Db 6 RSLRGRDAPAPTCPVAECFDLLVRHCVACGLLRTPRPKPAGASSPAPRTALQPOESVGA 65
 QY 63 --GSALRPDVALVGPALLGLILALTLVGLVSLVSWRWQ-QLRTAS----PDTSEGVQ 115
 Db 66 GAGEAALPLPGLLFGAPALLGLALVLAIV-LVGLVSWRWQRRLRGASSAEPDGDKDA- 123
 QY 116 QESLENVFPVSSETPHASAPTWPKEDADSALPRHSVPVPATELGSTELVTTKTAGEPQ 175
 Db 124 PEPLDKVILLSPG:SDATAPAWPPGPDGPTTPPGHSVPVPATELGSTELVTTKTAGEPQ 183

Search completed: February 5, 2004, 17:59:02
Job time : 37.4583 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 5, 2004, 18:00:55 ; Search time 29.1667 Seconds
(without alignments)
1256.294 Million cell updates/sec

Title: US-10-045-574B-28

Perfect score: 907
Sequence: 1 MGARRLRVRSQRSDSVPT.....PATELGSTELVTTKTAGEPQ 175

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
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- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09D_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
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- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	907	100.0	175	15	US-10-008-063-13
2	431.5	47.6	185	15	US-10-251-947-2
3	412	45.4	170	15	US-10-251-947-6
4	410.5	45.3	184	15	US-10-008-063-2
5	410.5	45.3	184	15	US-10-152-363A-60
6	401.5	44.3	171	15	US-10-251-947-4
7	401.5	44.3	171	15	US-10-251-947-7
8	395	43.6	186	15	US-10-251-947-14
9	150.5	16.6	328	15	US-10-008-063-42
10	116.5	12.8	181	9	US-09-854-864-5
11	116.5	12.8	184	12	US-10-216-074-11
12	116.5	12.8	184	12	US-10-087-080-39
13	116.5	12.8	184	14	US-10-077-438-1
14	116.5	12.8	184	14	US-10-077-438-7
15	116.5	12.8	184	14	US-10-077-137-1

16	116.5	12.8	184	14	US-10-077-137-7	Sequence 7, Appli
17	116.5	12.8	184	15	US-10-068-725-2	Sequence 2, Appli
18	116.5	12.8	184	15	US-10-151-882-47	Sequence 47, Appli
19	116.5	12.8	184	15	US-10-115-192-8	Sequence 8, Appli
20	116.5	12.8	184	15	US-10-008-063-7	Sequence 7, Appli
21	116.5	12.8	184	15	US-10-152-363A-27	Sequence 27, Appli
22	107	11.8	38	12	US-10-145-206-195	Sequence 195, App
23	102	11.2	839	12	US-10-237-496-54	Sequence 54, Appl
24	102	11.2	839	12	US-10-242-074-54	Sequence 54, Appl
25	102	11.2	839	12	US-10-242-505-54	Sequence 54, Appl
26	102	11.2	839	12	US-10-242-574-54	Sequence 54, Appl
27	102	11.2	839	12	US-10-243-261-54	Sequence 54, Appl
28	102	11.2	839	12	US-10-243-282-54	Sequence 54, Appl
29	102	11.2	839	12	US-10-243-402-54	Sequence 54, Appl
30	102	11.2	839	12	US-10-243-431-54	Sequence 54, Appl
31	102	11.2	839	12	US-10-245-164-54	Sequence 36, Appl
32	102	11.2	839	12	US-10-210-951-36	Sequence 54, Appl
33	102	11.2	839	12	US-10-244-972-54	Sequence 54, Appl
34	102	11.2	839	12	US-10-197-942-54	Sequence 36, Appl
35	102	11.2	839	12	US-10-211-884-36	Sequence 54, Appl
36	102	11.2	839	12	US-10-238-196-54	Sequence 54, Appl
37	102	11.2	839	12	US-10-245-013-54	Sequence 54, Appl
38	102	11.2	839	15	US-10-245-103-54	Sequence 54, Appl
39	102	11.2	839	15	US-10-245-107-54	Sequence 54, Appl
40	102	11.2	839	15	US-10-245-143-54	Sequence 54, Appl
41	102	11.2	839	15	US-10-245-771-54	Sequence 54, Appl
42	102	11.2	839	15	US-10-245-851-54	Sequence 54, Appl
43	102	11.2	839	15	US-10-245-883-54	Sequence 54, Appl
44	102	11.2	839	15	US-10-237-535-54	Sequence 54, Appl
45	102	11.2	839	15	US-10-238-183-54	Sequence 54, Appl

ALIGNMENTS

RESULT 1
US-10-008-063-13
; Sequence 13, Application US/1008063
; Publication No. US20030092164A1
; GENERAL INFORMATION:
; APPLICANT: Gross, Jane A.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Henne, Randal M. J.
; APPLICANT: Grant, Francis, J.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor
; FILE REFERENCE: 00-103
; CURRENT APPLICATION NUMBER: US/10/008,063
; CURRENT FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Mouse
US-10-008-063-13

Query Match	100.0%;	Score 907;	DB 15;	Length 175;
Best Local Similarity	100.0%;	Pred. No. 5.4e-81;		
Matches 175;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MGARRLRVRSQRSDSVPTQCNTQECFPLVNCVSCSELFHTPTDPTGHTSSLEPGTALQP	60	
Db	1	MGARRLRVRSQRSDSVPTQCNTQECFPLVNCVSCSELFHTPTDPTGHTSSLEPGTALQP	60	
Qy	61	QEGSALRPDVALIVGAPALLGLIALTLVGLVSLVSWRQQLRTASPTDSEGVOQESLE	120	
Db	61	QEGSALRPDVALIVGAPALLGLIALTLVGLVSLVSWRQQLRTASPTDSEGVOQESLE	120	
Qy	121	NVFPSETPHAPSAPTPWPKEDADSALPRHSPVPATLSTGLSTELVTTKTAGEPQ	175	
Db	121	NVFPSETPHAPSAPTPWPKEDADSALPRHSPVPATLSTGLSTELVTTKTAGEPQ	175	

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RESULT 2
US-10-251-947-2
; Sequence 2, Application US/10251947
; Publication No. US20030099990A1
; GENERAL INFORMATION:
; APPLICANT: Hsu, Hailing
; TITLE OF INVENTION: TALL-1 Receptor Molecules and Uses Thereof
; FILE REFERENCE: 01-1160-A
; CURRENT APPLICATION NUMBER: US/10/251,947
; CURRENT FILING DATE: 2002-09-20
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-251-947-2

Query Match      47.6%; Score 431.5; DB 15; Length 185;
Best Local Similarity 56.4%; Pred. No. 2.4e-34;
Matches 102; Conservative 10; Mismatches 54; Indels 15; Gaps 6;

QY 9 RSQRSDSSVPTQCNQTECFDPLVNCVSCLEFH--TPDT-GHTSSLEPGTALQPOE--- 62
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 6 RSLRGRDAPVTPCVPTQTECYDLLVRKVCDCRLLRKSPKTAAGASSPAPGTALQPOESVG 65
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 63 ---GSAALRPDVALLVGAPALLGLILALTLVGLVSLVSWRWQ--LR---TASPDTSQGV 114
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 66 TSGGEVSLPLPGLLFGAPALLGLVLLVLAIV-LVGLVSWRRQRRLRGAASTEAPDGDKAA 124
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 115 QESLENVFPVSSETPHASAPTWPLKEDADSLPRHSVPVPATELGSTELVTTKTAGPE 174
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 125 APEPLDKVILSPGTTDATAPAWPPGGDQGTTPPGHSIPVPATELGSTELVTTKTAGPE 184
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 175 Q 175
Db 185 Q 185

RESULT 3
US-10-251-947-6
; Sequence 6, Application US/10251947
; Publication No. US20030099990A1
; GENERAL INFORMATION:
; APPLICANT: Hsu, Hailing
; TITLE OF INVENTION: TALL-1 Receptor Molecules and Uses Thereof
; FILE REFERENCE: 01-1160-A
; CURRENT APPLICATION NUMBER: US/10/251,947
; CURRENT FILING DATE: 2002-09-20
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-251-947-6

Query Match      45.4%; Score 412; DB 15; Length 170;
Best Local Similarity 55.4%; Pred. No. 1.8e-32;
Matches 98; Conservative 9; Mismatches 48; Indels 22; Gaps 6;

QY 9 RSQRSDSSVPTQCNQTECFDPLVNCVSCLEFH--TPDTGHTSSLEPGTALQPOE--- 62
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 6 RSLRGRDAPVTPCVPTQTECYDLLVRKVCDCRLLRKSPKTAGASSPAPGTALQPOESVGT 65
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 63 ---GSAALRPDVALLVGAPALLGLILALTLVGLVSLVSWRWQ--LR-TASPDTSQGVQOES 118
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 66 GSGEVSLPLPGLLFGAPALLGLVLLVLAIV-LVGLVSWRRQRRLRGAASTEAPDG----- 119
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 119 LENVFPVSSETPHASAPTWPLKEDADSLPRHSVPVPATELGSTELVTTKTAGPEQ 175
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 120 -----DKAGTTDATAPAWPPGGDQGTTPPGHSIPVPATELGSTELVTTKTAGPEQ 170
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

```
RESULT 4
US-10-008-063-2
; Sequence 2, Application US/10008063
; Publication No. US20030092164A1
; GENERAL INFORMATION:
; APPLICANT: Gross, Jane A.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor
; FILE REFERENCE: 00-103
; CURRENT APPLICATION NUMBER: US/10/008,063
; CURRENT FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-008-063-2

Query Match      45.3%; Score 410.5; DB 15; Length 184;
Best Local Similarity 56.1%; Pred. No. 2.8e-32;
Matches 101; Conservative 9; Mismatches 55; Indels 15; Gaps 6;

QY 9 RSQRSDSSVPTQCNQTECFDPLVNCVSCLEFHT--PDTGHTSSLEPGTALQPOE--- 62
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 6 RSLRGRDAPVTPCVPAECFDLLVRHCVACGLLRTPRPKPAGASSPAPRTALQPOESVGA 65
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 63 --GSAALRPDVALLVGAPALLGLILALTLVGLVSLVSWRWQ--QLRTAS---PDTSEGVQ 115
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 66 GAGEAALPLPGLLFGAPALLGLVLLVLAIV-LVGLVSWRRQRRLRGASSAEAPDGDKDA- 123
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 116 QESLENVFPVSSETPHASAPTWPLKEDADSLPRHSVPVPATELGSTELVTTKTAGPEQ 175
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 124 PEPLDKVILSPGTSIDATAPAWPPGGDQGTTPPGHSVPVPATELGSTELVTTKTAGPEQ 183
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 5
US-10-152-363A-60
; Sequence 60, Application US/10152363A
; Publication No. US20030103986A1
; GENERAL INFORMATION:
; APPLICANT: Rixon, Mark W.
; TITLE OF INVENTION: TACI-Immunoglobulin Fusion Proteins
; FILE REFERENCE: 01-20
; CURRENT APPLICATION NUMBER: US/10/152,363A
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 60/293,343
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 60
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-152-363A-60

Query Match      45.3%; Score 410.5; DB 15; Length 184;
Best Local Similarity 56.1%; Pred. No. 2.8e-32;
Matches 101; Conservative 9; Mismatches 55; Indels 15; Gaps 6;

QY 9 RSQRSDSSVPTQCNQTECFDPLVNCVSCLEFHT--PDTGHTSSLEPGTALQPOE--- 62
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 6 RSLRGRDAPVTPCVPAECFDLLVRHCVACGLLRTPRPKPAGASSPAPRTALQPOESVGA 65
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 63 --GSAALRPDVALLVGAPALLGLILALTLVGLVSLVSWRWQ--QLRTAS---PDTSEGVQ 115
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 66 GAGEAALPLPGLLFGAPALLGLVLLVLAIV-LVGLVSWRRQRRLRGASSAEAPDGDKDA- 123
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 116 QESLENVFPVSSETPHASAPTWPLKEDADSLPRHSVPVPATELGSTELVTTKTAGPEQ 175
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 124 PEPLDKVILSPGTSIDATAPAWPPGGDQGTTPPGHSVPVPATELGSTELVTTKTAGPEQ 183
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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Db 124 PFPLDKVILSPGISDAPAWPPGGEDGTTTPGHSVPVPATELGS TELVTTKTAGPEQ 183

RESULT 6
US-10-251-947-4
; Sequence 4, Application US/10251947
; Publication No. US20030099990A1
; GENERAL INFORMATION:
; APPLICANT: Hsu, Hailing
; TITLE OF INVENTION: TALL-1 Receptor Molecules and Uses Thereof
; FILE REFERENCE: 01-1160-A
; CURRENT APPLICATION NUMBER: US/10/251,947
; CURRENT FILING DATE: 2002-09-20
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-251-947-4

Query Match 44.3%; Score 401.5; DB 15; Length 171;
Best Local Similarity 55.1%; Pred. No. 1.9e-31;
Matches 98; Conservative 9; Mismatches 48; Indels 23; Gaps 3

QY 9 RRSRSDSSVPTQCNOTECFDPVLRNCVSCBLFH--TPDT-GHTSSLEPGTALQPQE---62
Db 6 RSLRGDAPVPTPCVPTFCYDLLVRKVCDCRLLRKSPKTAAGASSPAPGTALQPQESVG 65
QY 63 ---GSAIRPDVALLVCAPALLGLIILALTGLVLSVSWRRQQLR-TASPDTSSEGVQOE 117
Db 66 TGSGEVSLPLPGLLFGAPALLGLVLVALV-LVGLVSWRRRQQLRCAASTEAPDG----120

QY 118 SLENVFPVSSETPHASAPTWPKEDADSALPRHSVPVPATELGSTELVTTKTAGPEQ 175
Db 121 -----DKAGTTDATAPAWPPGGEDGTTTPGHSIPVPATELGSTELVTTKTAGPEQ 171

RESULT 7
US-10-251-947-7
; Sequence 7, Application US/10251947
; Publication No. US20030099990A1
; GENERAL INFORMATION:
; APPLICANT: Hsu, Hailing
; TITLE OF INVENTION: TALL-1 Receptor Molecules and Uses Thereof
; FILE REFERENCE: 01-1160-A
; CURRENT APPLICATION NUMBER: US/10/251,947
; CURRENT FILING DATE: 2002-09-20
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-251-947-7

Query Match 44.3%; Score 401.5; DB 15; Length 171;
Best Local Similarity 55.1%; Pred. No. 1.9e-31;
Matches 98; Conservative 9; Mismatches 48; Indels 23; Gaps 3

QY 9 RRSRSDSSVPTQCNOTECFDPVLRNCVSCBLFH--TPDT-GHTSSLEPGTALQPQE---62
Db 6 RSLRGDAPVPTPCVPTFCYDLLVRKVCDCRLLRKSPKTAAGASSPAPGTALQPQESVG 65
QY 63 ---GSAIRPDVALLVCAPALLGLIILALTGLVLSVSWRRQQLR-TASPDTSSEGVQOE 117
Db 66 TGSGEVSLPLPGLLFGAPALLGLVLVALV-LVGLVSWRRRQQLRCAASTEAPDG----120

QY 118 SLENVFPVSSETPHASAPTWPKEDADSALPRHSVPVPATELGSTELVTTKTAGPEQ 175
Db 121 -----DKAGTTDATAPAWPPGGEDGTTTPGHSIPVPATELGSTELVTTKTAGPEQ 171

OTHER INFORMATION: "Xaa" can be any naturally occurring amino acid,
OTHER INFORMATION: or is absent.

FEATURE:

NAME/KEY: UNSURE

LOCATION: (134)

OTHER INFORMATION: "Xaa" can be any naturally occurring amino acid,
OTHER INFORMATION: or is absent.

FEATURE:

NAME/KEY: UNSURE

LOCATION: (135)

OTHER INFORMATION: "Xaa" can be any naturally occurring amino acid,
OTHER INFORMATION: or is absent.

FEATURE:

NAME/KEY: UNSURE

LOCATION: (136)

OTHER INFORMATION: "Xaa" can be any naturally occurring amino acid,
OTHER INFORMATION: or is absent.

FEATURE:

NAME/KEY: UNSURE

LOCATION: (137)

OTHER INFORMATION: "Xaa" can be any naturally occurring amino acid,
OTHER INFORMATION: or is absent.

FEATURE:

NAME/KEY: UNSURE

LOCATION: (138)

OTHER INFORMATION: "Xaa" can be any naturally occurring amino acid,
OTHER INFORMATION: or is absent.

US-10-251-947-14

Query Match 43.6%; Score 395; DB 15; Length 186;

Best Local Similarity 53.8%; Pred. No. 9.3e-31;

Matches 98; Conservative 8; Mismatches 60; Indels 16; Gaps 7;

QY 9 RSQRSDSSVPTQCNQTCSEFPLVNCVSCLEFH--TPDT-GHTSSLEPCTALQPOE---62

DB 6 RSLGRDAPVPTCPVPTTCICDILLVRKVCDCRLLRKSPKXAGASSPAPCTALQPOESVG65

QY 63 ---GSAIRPDVALLVGAPALLGLILALTGLVGLSVLSWRWQQ-LR---TASPDTSSEGV114

DB 66 TGSGEVSLPLPGLLRGAPALLGLVLAIV-LVGLSVLSWRWQQRLRGAASAPDGDGKAX124

QY 115 QOESLENVFPSE--TPHASAPTPPLKEDADSDALPRHSVPVPATELGSTELVTTKTAGP173

DB 125 XXXXXXXXXXGTTTATAPAMPFPGEDGQITTPGHSIPVPATELGSTELVTTKTAGP184

QY 174 EQ 175

DB 185 EQ 186

RESULT 9

US-10-008-063-42

Sequence 42, Application US/10008063

Publication No. US20030092164A1

GENERAL INFORMATION:

APPLICANT: Gross, Jane A.

APPLICANT: Xu, Wenfeng

APPLICANT: Henne, Randal M.

APPLICANT: Grant, Francis, J.

TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor

FILE REFERENCE: 00-103

CURRENT APPLICATION NUMBER: US/10/008,063

CURRENT FILING DATE: 2001-11-05

NUMBER OF SEQ ID NOS: 46

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 42

LENGTH: 328

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Ztnfr12-tcs-FC5.

US-10-008-063-42

Query Match 16.8%; Score 150.5; DB 15; Length 328;

Best Local Similarity 31.2%; Pred. No. 1.8e-06;

Matches 54; Conservative 11; Mismatches 57; Indels 51; Gaps 6;

QY 9 RSQRSDSSVPTQCNQTCSEFPLVNCVSCLEFHT--PDTGHTSSLEPCTALQPOEGSAL66

DB 25 RSLGRDAPVPTCPVPAECFDDLLVRICVACGLLRTPRPKPCAGASSPAPCTALQPOES---81

QY 67 RPDVALLVGAPALLGLILALTGLVGLSVLSWRWQQRLRTASPDTSSEGVQOESLENVFPVS126

DB 82 -----VGAGA-----GEAALV-----PRGSE-----PKS100

QY 127 SETPHASAPTPPLKEDADSDAL-----PRHSVPVPATELGSTELVTTKTAGPE174

DB 101 SDKHTCCPCPAPEAGAPSVFLPPKPKDITLMISETPEVTCVVVDVSHEDPE153

RESULT 10

US-09-854-864-5

Sequence 5, Application US/09854864

Patent No. US20020081296A1

GENERAL INFORMATION:

APPLICANT: THEILL, LARS EYDE

APPLICANT: YU, GANG

TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCVA,

FILE REFERENCE: A-6863

CURRENT APPLICATION NUMBER: US/09/854,864

CURRENT FILING DATE: 2001-09-11

PRIOR APPLICATION NUMBER: US 60/204,039

PRIOR FILING DATE: 2000-05-12

PRIOR APPLICATION NUMBER: US 60/214,591

PRIOR FILING DATE: 2000-06-27

NUMBER OF SEQ ID NOS: 31

SOFTWARE: PatentIn version 3.1

SEQ ID NO 5

LENGTH: 181

TYPE: PRT

ORGANISM: Homo sapiens

US-09-854-864-5

Query Match 12.8%; Score 116.5; DB 9; Length 181;

Best Local Similarity 29.4%; Pred. No. 0.0018;

Matches 50; Conservative 21; Mismatches 64; Indels 35; Gaps 8;

QY 21 QCNQTECFDPLVNCVSCLEFHTPDTGHTSSLEPCTALQPOEGSALRPDVALLVGAPALL80

DB 4 QCSQNEYFDSLHACIPQQL-----RCSNTPPLTCQRYCNASVTSVK---GTNAIL53

QY 81 GLILALTGLVGLSVLSWRWQQRLRTASPDTSSEGVQOE-----SLENVFPVPSSET--129

DB 54 WTCGLSLI--ISLAVFLMFLRKIS---SEPLKDEFKNTGSGLLGMANIDLEKSRGCD108

QY 130 ----PHASAPTPPLK-EDADSALPR-----HSVPVPATELGSTELVTTKT170

DB 109 EIIILPRGLEVTBECTCEDCICKPKVDSHCPPLPAMEBEGATILVTTKT158

RESULT 11

US-10-216-074-11

Sequence 11, Application US/10216074

Publication No. US2003014845A1

GENERAL INFORMATION:

APPLICANT: Shu, Hong-Bing

TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND

METHODS OF USE THEREOF

FILE REFERENCE: 2879-72

CURRENT APPLICATION NUMBER: US/10/216,074

CURRENT FILING DATE: 2003-03-12

PRIOR APPLICATION NUMBER: US/09/565,423

PRIOR FILING DATE: 2000-05-05

PRIOR APPLICATION NUMBER: UNKNOWN

PRIOR FILING DATE: 2000-05-01

; PRIOR APPLICATION NUMBER: 60/132,892
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 11
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-077-438-1
; Sequence 1, Application US/10077438
; Publication No. US20020165156A1
; GENERAL INFORMATION:
; APPLICANT: Mackay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc. S.A.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,438
; PRIOR FILING DATE: 2002-02-18
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-438-1
Query Match 12.8%; Score 116.5; DB 12; Length 184;
Best Local Similarity 29.4%; Pred. No. 0.0019;
Matches 50; Conservative 21; Mismatches 64; Indels 35; Gaps 8;
QY 21 QCNQTECFDPLVNCVSCLEFHTPTDGTHTSSLEPCTALQPOEGSALRPDVALLVGPALL 80
DB 7 QCSQNEFYDLSLHACIPCOL-----RCSNTPPLTCQRYCNASVTNSVK---GTNAIL 56
QY 81 GLILALTLVGLSVSWRWQRLRTASPTDTSSEGVQOE-----SLENVFPVSSET-- 129
DB 57 WTCLGLSLI--ISLAVFVLMFLRKIS---SEPLKDFKNTGSGLLGWNIDLEKSRGTD 111
QY 130 ----PHASAPTWPLK-EDADSALPR-----HSVPVPATELGSTELVTTKT 170
DB 112 EIILPRGLETVVECTCEDCIKSPKVDSDHCFPLPAMEGATILVTTKT 161
RESULT 12
US-10-087-080-39
; Sequence 39, Application US/10087080
; Publication No. US20030235820A1
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Eos Biotechnology, Inc.
; APPLICANT: Case Western Reserve University
; TITLE OF INVENTION: No. US20030235820A1 Methods of Diagnosis of Metastatic Colorectal
; TITLE OF INVENTION: Cancer, Compositions and Methods of Screening for
; TITLE OF INVENTION: Modulators of Metastatic Colorectal Cancer
; FILE REFERENCE: 018501-000840US
; CURRENT APPLICATION NUMBER: US/10/087,080
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 60/272,206
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: US 60/281,149
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US 60/284,555
; PRIOR FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 39
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: tumor necrosis factor receptor superfamily, member
; OTHER INFORMATION: 17 (TNFRSF17)
US-10-087-080-39
Query Match 12.8%; Score 116.5; DB 12; Length 184;
Best Local Similarity 29.4%; Pred. No. 0.0019;
Matches 50; Conservative 21; Mismatches 64; Indels 35; Gaps 8;
QY 21 QCNQTECFDPLVNCVSCLEFHTPTDGTHTSSLEPCTALQPOEGSALRPDVALLVGPALL 80
DB 7 QCSQNEFYDLSLHACIPCOL-----RCSNTPPLTCQRYCNASVTNSVK---GTNAIL 56
QY 81 GLILALTLVGLSVSWRWQRLRTASPTDTSSEGVQOE-----SLENVFPVSSET-- 129
DB 57 WTCLGLSLI--ISLAVFVLMFLRKIS---SEPLKDFKNTGSGLLGWNIDLEKSRGTD 111
QY 130 ----PHASAPTWPLK-EDADSALPR-----HSVPVPATELGSTELVTTKT 170

DB 112 EIILPRGLETVVECTCEDCIKSPKVDSDHCFPLPAMEGATILVTTKT 161
RESULT 13
US-10-077-438-1
; Sequence 1, Application US/10077438
; Publication No. US20020165156A1
; GENERAL INFORMATION:
; APPLICANT: Mackay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc. S.A.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,438
; PRIOR FILING DATE: 2002-02-18
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-438-1
Query Match 12.8%; Score 116.5; DB 14; Length 184;
Best Local Similarity 29.4%; Pred. No. 0.0019;
Matches 50; Conservative 21; Mismatches 64; Indels 35; Gaps 8;
QY 21 QCNQTECFDPLVNCVSCLEFHTPTDGTHTSSLEPCTALQPOEGSALRPDVALLVGPALL 80
DB 7 QCSQNEFYDLSLHACIPCOL-----RCSNTPPLTCQRYCNASVTNSVK---GTNAIL 56
QY 81 GLILALTLVGLSVSWRWQRLRTASPTDTSSEGVQOE-----SLENVFPVSSET-- 129
DB 57 WTCLGLSLI--ISLAVFVLMFLRKIS---SEPLKDFKNTGSGLLGWNIDLEKSRGTD 111
QY 130 ----PHASAPTWPLK-EDADSALPR-----HSVPVPATELGSTELVTTKT 170
DB 112 EIILPRGLETVVECTCEDCIKSPKVDSDHCFPLPAMEGATILVTTKT 161
RESULT 14
US-10-077-438-7
; Sequence 7, Application US/10077438
; Publication No. US20020165156A1
; GENERAL INFORMATION:
; APPLICANT: Mackay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,438
; PRIOR FILING DATE: 2002-02-18
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684

Db 112 EILPRGLEVTVECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKT 161
Search completed: February 5, 2004, 18:09:54
Job time : 30.1667 secs

Query Match 12.8%; Score 116.5; DB 14; Length 184;
Best Local Similarity 29.4%; Pred. No. 0.0019;
Matches 50; Conservative 21; Mismatches 64; Indels 35; Gaps 8;
QY 21 QCNQTECFDPLVRNCVSCELFHTPTDGTGHTSLEPGTALQPOEGSALRPDPVALLVGAPALL 80
Db 7 QCSQNEYFDSLHACIPCOL-----RCSNTPPLTCQRYCNASVTSVK---GTNAIL 56
QY 81 GLILALTUVLVSLVSWRWQRLRTASPDTSSEGVQOE-----SLENVFPSET-- 129
Db 57 WTCGLSLI--ISLAVFVLMFLRKIS---SEPLKDFKNTGSGLLGMANIDLEKSRGTD 111
QY 130 ----PHASAPTWPLK-EDADSALPR----HSVPVPATELSTELVTTKT 170
Db 112 EILPRGLEVTVECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKT 161

RESULT 15
US-10-077-137-1
; Sequence 1, Application US/10077137
; Publication No. US20020172674A1
; GENERAL INFORMATION:
; APPLICANT: Mackay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschoopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Adotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; TITLE OF INVENTION: Immunoregulatory Agent
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077.137
; CURRENT FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-137-1

Query Match 12.8%; Score 116.5; DB 14; Length 184;
Best Local Similarity 29.4%; Pred. No. 0.0019;
Matches 50; Conservative 21; Mismatches 64; Indels 35; Gaps 8;
QY 21 QCNQTECFDPLVRNCVSCELFHTPTDGTGHTSLEPGTALQPOEGSALRPDPVALLVGAPALL 80
Db 7 QCSQNEYFDSLHACIPCOL-----RCSNTPPLTCQRYCNASVTSVK---GTNAIL 56
QY 81 GLILALTUVLVSLVSWRWQRLRTASPDTSSEGVQOE-----SLENVFPSET-- 129
Db 57 WTCGLSLI--ISLAVFVLMFLRKIS---SEPLKDFKNTGSGLLGMANIDLEKSRGTD 111
QY 130 ----PHASAPTWPLK-EDADSALPR----HSVPVPATELSTELVTTKT 170

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OM protein - protein search, using sw model

Run on: February 5, 2004, 17:57:39 ; Search time 14.0972 Seconds
(without alignments)
525.238 Million cell updates/sec

Title: US-10-045-574B-28

Perfect score: 907

Sequence: 1 MGARRLRVRSQRSDSSVPT.....PATELGSTELVTTKTAGEQ 175

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:**

- 1: /cgn2_6/ptodata/1/iaa/5A COMB.pap.*
- 2: /cgn2_6/ptodata/1/iaa/5B COMB.pap.*
- 3: /cgn2_6/ptodata/1/iaa/6A COMB.pap.*
- 4: /cgn2_6/ptodata/1/iaa/6B COMB.pap.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pap.*
- 6: /cgn2_6/ptodata/1/iaa/backfilesl.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	116.5	12.8	184	4	US-09-565-423-11
2	101.5	11.2	185	4	US-09-565-423-17
3	94	10.4	265	4	US-09-322-409-49
4	94	10.4	265	4	US-09-451-527-49
5	94	10.4	291	4	US-09-322-409-44
6	94	10.4	291	4	US-09-451-527-44
7	94	10.4	1384	3	US-08-976-255-11
8	86.5	9.5	365	4	US-09-252-991A-30595
9	85.5	9.4	913	1	US-08-445-640-4
10	85.5	9.4	913	3	US-08-170-558-4
11	85.5	9.4	913	3	US-08-447-314-4
12	85.5	9.4	913	3	US-08-445-461-4
13	85.5	9.4	913	1	US-08-336-343A-2
14	83	9.2	750	4	US-09-165-239A-4
15	82.5	9.1	499	3	US-09-049-672A-1
16	81	8.9	319	3	US-08-630-172-12
17	81	8.9	319	3	US-09-375-419-12
18	81	8.9	574	4	US-08-484-970B-172
19	80	8.8	379	1	US-08-250-859-2
20	80	8.8	379	1	US-08-347-029-2
21	80	8.8	379	1	US-08-490-803-2
22	80	8.8	379	1	US-08-484-246-2
23	80	8.8	379	2	US-08-457-254-2
24	80	8.8	379	3	US-08-999-927-4
25	80	8.8	379	4	US-08-461-819-4
26	80	8.8	379	5	PCT-US94-08806-2
27	80	8.8	379	5	PCT-US93-01775-2

28 80 8.8 379 5 PCT-US95-01829-4 Sequence 4, Appli
29 80 8.8 379 5 PCT-US95-14932-2 Sequence 2, Appli
30 80 8.8 379 5 PCT-US95-16626-2 Sequence 2, Appli
31 79.5 8.8 486 4 US-09-252-991A-22482 Sequence 22482, A
32 79 8.7 361 4 US-09-252-991A-30426 Sequence 30426, A
33 78.5 8.7 192 1 US-08-086-428B-61 Sequence 61, Appl
34 78.5 8.7 192 2 US-08-468-570-61 Sequence 61, Appl
35 78.5 8.7 192 2 US-08-290-665A-61 Sequence 61, Appl
36 78.5 8.7 192 4 US-08-466-601A-61 Sequence 61, Appl
37 78.5 8.7 192 5 PCT-US95-10398-61 Sequence 61, Appl
38 78.5 8.7 1942 4 US-09-252-991A-30444 Sequence 30444, A
39 78 8.6 249 3 US-09-105-343A-2 Sequence 2, Appli
40 78 8.6 552 1 US-07-999-280A-22 Sequence 22, Appl
41 78 8.6 552 1 US-07-999-280A-24 Sequence 24, Appl
42 78 8.6 552 1 US-08-426-279-22 Sequence 22, Appl
43 78 8.6 552 1 US-08-426-279-24 Sequence 24, Appl
44 78 8.6 552 1 US-08-401-013-22 Sequence 22, Appl
45 78 8.6 552 1 US-08-401-013-24 Sequence 24, Appl

ALIGNMENTS

RESULT 1
US-09-565-423-11
; Sequence 11, Application US/09565423
; Patent No. 6475987
; GENERAL INFORMATION:
; APPLICANT: Shu, Hong-Bing
; TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
; FILE REFERENCE: 2879-72
; CURRENT APPLICATION NUMBER: US/09/565,423
; CURRENT FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: UNKNOWN
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/132,892
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-565-423-11

Query Match 12.8%; Score 116.5; DB 4; Length 184;
Best Local Similarity 29.4%; Pred. No. 0.00022;
Matches 50; Conservative 21; Mismatches 64; Indels 35; Gaps 8;
QY 21 QCNQTECFDPLVNCVSCELFTPTDGTGHTSSLEPGTALQPEGSLALPDVALLVCAPALL 80
Db 7 QCSQNEYFDSLHACIPCOL-----RCSNTPFLTQRYCNASVTNSVK---GTMAIL 56
QY 81 GLLIALTLGLVLSWRWRQRLTASPTSGVQOE-----SLENVFPSET-- 129
Db 57 WTCLGLSLI--ISLAVFLMFLLRKIS---SPLKDEPKNTGSLGLGWANIDLEKSRGTD 111
QY 130 -----PHASAPTWPLK-EDADSALPR-----HVPVPATLGGSTELVTTKT 170
Db 112 EILIPRGLEYTVBECTCEDCIKSPKVDSDHCFPLPAMEGATILVTTKT 161

RESULT 2
US-09-565-423-17
; Sequence 17, Application US/09565423
; Patent No. 6475987
; GENERAL INFORMATION:
; APPLICANT: Shu, Hong-Bing
; TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
; FILE REFERENCE: 2879-72
; CURRENT APPLICATION NUMBER: US/09/565,423

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; CURRENT FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: UNKNOWN
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/132,892
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 17
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-565-423-17

Query Match
Best Local Similarity 11.2%; Score 101.5; DB 4; Length 185;
Matches 53; Conservative 14; Mismatches 60; Indels 53; Gaps 9;

QY 21 QCNQTECDPLVRNCVSCLEHTDTGHTSSLEPGTALQPEGSALEPVDVALLV-CAPAL 79
DB 4 QCFHSEYFDSLHACKPC-----HLRCSNPATCQY-----CDPSVTSSVKGTYY 50
QY 80 LGLILALTLVGLVSL--VSWRWQQLRTA-----SPDTSEGVQQ-----116
DB 51 LWIFLGLTLVLSLALFTISFLRKNMPEALKDEPQSPQLDGSQAQLDKADTELTRIRAGD 110
QY 117 -----ESLE-NVFPVSSSTPHASAPTPPEPKEDADSLPRHSVPVPATELGSTELVTTKT 170
DB 111 DRIFPRSLYEYVECTDCVKSKP-----KGDSD-----HFFPLPAMEEGATILVTTKT 160

RESULT 3
US-09-322-409-49
; Sequence 49, Application US/09322409
; Patent No. 6471957
; GENERAL INFORMATION:
; APPLICANT: Yang, Gek-Kee
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/09/322,409
; CURRENT FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 49
; LENGTH: 265
; TYPE: PRT
; ORGANISM: Felis catus
US-09-322-409-49

Query Match
Best Local Similarity 10.4%; Score 94; DB 4; Length 265;
Matches 42; Conservative 11; Mismatches 59; Indels 32; Gaps 7;

QY 33 RNCVSC-ELFHTPTDGTGHTSSLEPGTALQPEGSALEPVDVALLVGPALLGLIL---ALTL 88
DB 122 RNFGCLLEQCQPD-----STPLPRSPRALEATAPAPQAPLILLILLPVALLL 173
QY 89 VGLVLSVSW---RW-----RQQLRTASP-----DTSEGVQESLENVFPVSPSTPHA 132
DB 174 MSAANCLHRRRRWRTPTVPRQKTLRPRRNHLPTDETFGLGESQLET-----GSFLDHA 229
QY 133 SAPTWPEPKEDADSLPRHSVPVP 156
DB 230 APLTLPPGWRQRPPTPADPPIP 253

RESULT 4
US-09-451-527-49
; Sequence 49, Application US/09451527
; Patent No. 6482403
; GENERAL INFORMATION:
; APPLICANT: Yang, Gek-Kee
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/09/451,527
; CURRENT FILING DATE: 1999-12-01
; EARLIER APPLICATION NUMBER: 09/322,409
; EARLIER FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 49
; LENGTH: 265
; TYPE: PRT
; ORGANISM: Felis catus
US-09-451-527-49

Query Match
Best Local Similarity 10.4%; Score 94; DB 4; Length 265;
Matches 42; Conservative 11; Mismatches 59; Indels 32; Gaps 7;

QY 33 RNCVSC-ELFHTPTDGTGHTSSLEPGTALQPEGSALEPVDVALLVGPALLGLIL---ALTL 88
DB 122 RNFGCLLEQCQPD-----STPLPRSPRALEATAPAPQAPLILLILLPVALLL 173
QY 89 VGLVLSVSW---RW-----RQQLRTASP-----DTSEGVQESLENVFPVSPSTPHA 132
DB 174 MSAANCLHRRRRWRTPTVPRQKTLRPRRNHLPTDETFGLGESQLET-----GSFLDHA 229
QY 133 SAPTWPEPKEDADSLPRHSVPVP 156
DB 230 APLTLPPGWRQRPPTPADPPIP 253

RESULT 5
US-09-322-409-44
; Sequence 44, Application US/09322409
; Patent No. 6471957
; GENERAL INFORMATION:
; APPLICANT: Yang, Gek-Kee
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/09/322,409
; CURRENT FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 44
; LENGTH: 291
; TYPE: PRT
; ORGANISM: Felis catus
US-09-322-409-44

Query Match
Best Local Similarity 10.4%; Score 94; DB 4; Length 291;
Matches 42; Conservative 11; Mismatches 59; Indels 32; Gaps 7;

QY 33 RNCVSC-ELFHTPTDGTGHTSSLEPGTALQPEGSALEPVDVALLVGPALLGLIL---ALTL 88
DB 148 RNFGCLLEQCQPD-----STPLPRSPRALEATAPAPQAPLILLILLPVALLL 199
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QY 89 VGLVSLVSW---RW-----RQQLRTASP-----DTSEGVQOESLENVFPSSSTPHA 132
Db 200 MSAACWCLHWRRRWTPYPREQKTLRPRRNHLPEDTEPGIGESQLET-----GSFLDHA 255
QY 133 SAPTWPLKEDADALSALPHSVVP 156
Db 256 APLTLPFGWRQRPPTAPDPPIP 279

RESULT 6

US-09-451-527-44
; Sequence 44, Application US/09451527
; Patent No. 6482403
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wondersling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/09/451,527
; CURRENT FILING DATE: 1999-12-01
; EARLIER APPLICATION NUMBER: 09/322,409
; EARLIER FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 44
; LENGTH: 291
; TYPE: PRT
; ORGANISM: Felis catus
US-09-451-527-44

Query Match 10.4%; Score 94; DB 4; Length 291;
Best Local Similarity 29.2%; Pred. No. 0.086;
Matches 42; Conservative 11; Mismatches 59; Indels 32; Gaps 7;
QY 33 RNCVSC-ELFHTPDTHGTSLSLEPGTALOPQEGSALRPDVALLVGAPALLGLIL---ALTL 88
Db 148 RNFSGCLELCCQDS-----STPLPRSPRALENTALPAQAPLILLLLLLPVALL 199
QY 89 VGLVSLVSW---RW-----RQQLRTASP-----DTSEGVQOESLENVFPSSSTPHA 132
Db 200 MSAACWCLHWRRRWTPYPREQKTLRPRRNHLPEDTEPGIGESQLET-----GSFLDHA 255
QY 133 SAPTWPLKEDADALSALPHSVVP 156
Db 256 APLTLPFGWRQRPPTAPDPPIP 279

RESULT 7

US-08-976-255-11
; Sequence 11, Application US/08976255
; Patent No. 6136581
; GENERAL INFORMATION:
; APPLICANT: Jono, Keith E.
; APPLICANT: Plowman, Gregory
; TITLE OF INVENTION: KINASE GENES AND USES
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/976,255
; FILING DATE: No. 6136581ember 21, 1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/031,675
; FILING DATE: No. 6136581ember 22, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 229/182
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1384 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
US-08-976-255-11
Query Match 10.4%; Score 94; DB 3; Length 1384;
Best Local Similarity 26.5%; Pred. No. 0.74;
Matches 54; Conservative 23; Mismatches 79; Indels 48; Gaps 10;
QY 1 MGARL-----RVRSQRGRDSSVPQCNCQTCFDPVLVNCVSCBELFHTPTDGTGTSLSLEPGT 56
Db 677 VGARAAQRGHRWSNVSNANNSGSRG--PESWDVFSAGC-HAEGCPSKQTPRASPEPGY 733
QY 57 ALQP-----QEGSALRPDVALLVGAPALLGLILALTVLGLVSLVSWRWQ----- 101
Db 734 PGEPLILGLQAASAEQPGC-----CPGLPHLCSAQGLAPCLVTPSTTETASSGGDHPQA 788
QY 102 --QLRTASPDTS-----EGVQOESLENVFPSSSTPHASAPTWPFLKEDADALSALPHSV 153
Db 789 EPKLATEAGTTPRLPLPSVPSQEGALPSEB---ASAP-----DAPDALPDSPT 838
QY 154 PVPATELGLSTELVTI---KTAGPE 174
Db 839 PATGGEVSAIKLASALNGSSSPE 862

RESULT 8

US-09-252-991A-30595
; Sequence 30595, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30595
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30595

Query Match 9.5%; Score 86.5; DB 4; Length 365;
Best Local Similarity 27.5%; Pred. No. 0.7;
Matches 44; Conservative 15; Mismatches 74; Indels 27; Gaps 7;

Qy	16	SSVPTCQCITECDFLVRNCVSCSLFTPTDGTGHTSSLEPG--TALQP--QEGSALRPDVA	71
Db	27	STAPSCRAISLSSPDR--VEGE-----PSHGKGPLRRGRRTAIIACLNAGGETVPAHR	80
Qy	72	LIVGAPALLGLIATLVLGLVLSVSRWROQLRTASPTDTEGVQOQSLE-----	120
Db	81	LIAGARDIIEORRAFTLGANQITSWLPQPLPAAFSRDELLETTPPREPAPVPRARA	140
Qy	121	----NVFVPSSTPHASAPTTPPKEDADSLPRHSVPVP	156
Db	141	IDAPQARVQAEAP--ASAPSVAPAAPVEGRGIP--ISLPKP	178

RESULT 9
US08-445-640-4
; sequence 4, Application US/08445640
; Patent No. 5709858
; GENERAL INFORMATION:
; APPLICANT: Godowski, Paul J.
; APPLICANT: Mark, Melanie R.
; APPLICANT: Scadden, David T.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Baron, Will F.
; TITLE OF INVENTION: Protein Tyrosine Kinases
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

```

Query Match      9.4%; Score 85.5; DB 1; Length 913;
Best Local Similarity 30.2%; Pred. No. 3.1;
Matches 39; Conservative 19; Mismatches 38; Indels 33; Gaps 10;

Qy 44 PQTGHTSLSEPTALQPC-----EGSALRPDVALVGPALGLIALTLVLVSLV 95
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 390 PPPTNFSSLE-----LEPRGQFVAKPGS-----PTAILG--CLVAIIILLLL--IALL 437

Qy 96 SWR--WRQQLRTASPDTSSEGVQQSLSLNVFVS-----SETHAGAPTWPKEDADSAL 148
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 438 LWLHLWRLLSKAE---RRVLEESLTVHLSVPGDITLNNRPGPREP---PPVQGPFRPRGN 492

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Qy	149	PRHSVP-VP	156
Db	493	PpHSAPCVP	501

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Query Match      9.4%; Score 85.5; DB 3; Length 913;
Best Local Similarity 30.2%; Pred. No. 3.1;
Matches 39; Conservative 19; Mismatches 38; Indels 33; Gaps 10;

QY      44 PQTGHTSLEPGTALQ-----EGSALRPDVALVAPALLGLIATLTGLVSLV 95
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      390 PPPTNFSSLE-----LEPRGQOPVAKPEG-----PTRLIG--CLVAIIILLILI--TALM 437

QY      96 SWR--WRQLRATSPDTSEGVQGESLENVFVPS-----SETPHASAPTWPLKEDASAL 148
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      438 LARLHWRLLSKAE--RRVLEEELTVHLSVPGDTILINNRGPGPREP--PPVQPRPGRN 492

QY      149 PRHSVP-VP 156
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Db      493 PPHSAPCPVP 501
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RESULT 11
US-08-447-314-4
; Sequence 4, Application US/08447314
; Patent No. 6087144

GENERAL INFORMATION:
APPLICANT: Scadden, David T.
APPLICANT: Baker, Kevin P.
APPLICANT: Baron, Will F.
TITLE OF INVENTION: Protein Tyrosine Kinases
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/447,314
FILING DATE: 22-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/170558
FILING DATE: 20-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/157563
FILING DATE: 23-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 854CID2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/425-1896
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 913 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-447-314-4

Query Match 9.4%; Score 85.5; DB 3; Length 913;
Best Local Similarity 30.2%; Pred. No. 3.1;
Matches 39; Conservative 19; Mismatches 38; Indels 33; Gaps 10;

Qy 44 PDTGHTSSLEPGTALQPO-----EGSALRPDVALVGPALLGLILALTIVGLVSLV 95
Db 390 PPPTNFSLE-----LEPRGQQPVAKPEGS-----PTAILIG--CLVAIILLILLI--IALM 437

Qy 96 SWR--WRQQLRTASPDTSRGVQESLENVFPVS-----SETPHASAPTWPLPKEDADSAL 148
Db 438 LWRHLWRLLSKAE--RRVLEELTVHLSVPGDTILINNRPGPREP--PPYQEPRPGRN 492

Qy 149 PRHSVP-VP 156
Db 493 PPHSAPCPV 501

RESULT 12
US-08-445-461-4
Sequence 4, Application US/08445461
Patent No. 6096527
GENERAL INFORMATION:
APPLICANT: Godowski, Paul J.
APPLICANT: Mark, Melanie R.
APPLICANT: Scadden, David T.
APPLICANT: Baker, Kevin P.
APPLICANT: Baron, Will F.
TITLE OF INVENTION: Protein Tyrosine Kinases
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/445,461
FILING DATE: 22-MAY-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/170558
FILING DATE: 20-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/157563
FILING DATE: 23-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 854C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 913 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-445-461-4

Query Match 9.4%; Score 85.5; DB 3; Length 913;
Best Local Similarity 30.2%; Pred. No. 3.1;
Matches 39; Conservative 19; Mismatches 38; Indels 33; Gaps 10;

Qy 44 PDTGHTSSLEPGTALQPO-----EGSALRPDVALVGPALLGLILALTIVGLVSLV 95
Db 390 PPPTNFSLE-----LEPRGQQPVAKPEGS-----PTAILIG--CLVAIILLILLI--IALM 437

Qy 96 SWR--WRQQLRTASPDTSRGVQESLENVFPVS-----SETPHASAPTWPLPKEDADSAL 148
Db 438 LWRHLWRLLSKAE--RRVLEELTVHLSVPGDTILINNRPGPREP--PPYQEPRPGRN 492

Qy 149 PRHSVP-VP 156
Db 493 PPHSAPCPV 501

RESULT 13
US-08-336-343A-2
Sequence 2, Application US/08336343A
Patent No. 5677144
GENERAL INFORMATION:
APPLICANT: Ullrich, Axel
APPLICANT: Alves, Frauke
TITLE OF INVENTION: CCK-2, A No. 5677144el Receptor Tyrosine Kinase
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/336.343A

FILING DATE: 08-NOV-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7683-065

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 869-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 919 amino acids

TYPE: amino acid

TOPOLOGY: unknown

MOLECULE TYPE: protein

US-08-336-343A-2

Query Match 9.4%; Score 85.5; DB 1; Length 919;

Best Local Similarity 30.2%; Pred. No. 3.1;

Matches 39; Conservative 19; Mismatches 38; Indels 33; Gaps 10;

QY 44 PDTGHTSSLEPGTALQPO-----EGSALRPDVALLGAPALLGILALTLVGLVSLV 95

Db 390 PPTNFFSLE-----LEPGQOPVAKAGS-----PTALIG--CLVAIIILLILI--IALM 437

QY 96 SWR--WRQLRTASPDTSSEGVQCSLENVFPVS-----SETPHASAPTPWPKEDADSAL 148

Db 438 LWRLHWRLLSKAE---RRVLEELTVHLSVPGDTILINRPGPREP--PPVQEPFRGN 492

QY 149 PHSVVP-VP 156

Db 493 PPHSAPCPV 501

RESULT 14

US-09-165-239A-4

Sequence 4, Application US/09165239A

Patent No. 6344554

GENERAL INFORMATION:

APPLICANT: JOHNSON, ALEXANDER

APPLICANT: BRAUN, BURKHARD R

TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCES FROM CANDIDA

TITLE OF INVENTION: ALBICANS ENCODING POLYPEPTIDES ASSOCIATED WITH FILAMENTOUS

TITLE OF INVENTION: GROWTH

FILE REFERENCE: 22002200700

CURRENT APPLICATION NUMBER: US/09/165.239A

CURRENT FILING DATE: 1998-10-01

PRIOR APPLICATION NUMBER: 60/068,065

PRIOR FILING DATE: 1997-12-18

NUMBER OF SEQ ID NOS: 13

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 4

LENGTH: 750

TYPE: PRT

ORGANISM: Candida albicans

US-09-165-239A-4

Query Match

Best Local Similarity 33.9%; Pred. No. 4.3;

Matches 21; Conservative 6; Mismatches 35; Indels 0; Gaps 0;

QY 110 TSEGVQCSLENVFPVSSETPHASPWPKEDADALPRHVPVPAVELGSELVTTK 169

Db 351 TPESAPETTPESAPESVPESAPETTPESAPESVPESAPETTTPTTAHLTTT 410

QY 170 TA 171

Db 411 TA 412

RESULT 15

US-09-049-672A-1

Sequence 1, Application US/09049672A

Patent No. 6135941

GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.

APPLICANT: Lal, Preeti

APPLICANT: Tang, Y. Tom

APPLICANT: Yue, Henry

APPLICANT: Au-Young, Janice

APPLICANT: Corley, Neil C.

APPLICANT: Guegler, Karl J.

APPLICANT: Baughn, Marian R.

TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESS: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/049,672A

FILING DATE: HEREWITH

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Cerrone, Michael C

REGISTRATION NUMBER: 39,132

REFERENCE/DOCKET NUMBER: PF-0497 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-855-0555

TELEFAX: 650-845-4166

TELEX:

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 499 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: ADENINE01

CLONE: 021145

US-09-049-672A-1

Query Match 9.1%; Score 82.5; DB 3; Length 499;

Best Local Similarity 25.3%; Pred. No. 2.8;

Matches 48; Conservative 18; Mismatches 65; Indels 59; Gaps 11;

QY 20 TQCNQTECFDPLVRNCVSCLELPH-----TPDTGHTSSLEPGCTALQPOEGSAL 66

Db 221 TQC-----LAGKSVTCHVKHYTNPSQDVTVPVPTPTPTPS--PSTPTPTSP--SCC 269

QY 67 RPDVALLVGAPALLGLI-----LALTVLGL--VSLVSMWRQQLRTASPDTSSEGVQOES 118

Db 270 HPRLSL--HRPALEDILLGSEANLTCITLGLDASGVFTWTP---SSGKSAVQGPPEPD 324

QY 119 LENFVPSSTPHASAPTW-----PPLKEDADSALPR-----HSPVPA 157

Db 325 LCGCYSVSSVLPSCAQP--WNHGETFTCTAAHPELKTPLTANITKSGNTFRPEVHLLPPPS 383

QY 158 TELGSTELVT 167

Db 384 EELALNELVT 393

Search completed: February 5, 2004, 18:02:10
Job time : 15.0972 secs
